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Genetic Analysis of Amylographic Viscosity Measurements of Milled Rice by Means of Diallel Graph[1]

Yih-Chuan Kuo[2], Bill D. Webb[3] and James W. Stansel[4]

Abstract : Amylographic viscosity measurements, a physical property of milled rice flour, are important eating and processing quality parameters of rice and are characteristics of the endosperm. A genetic study on amylographic viscosity measurements of milled rice flour by means of diallel graph was conducted. An additive-dominance model with independence of the genes in action and in distribution is demonstrated by the excellent unit-slope linearity for all viscosity measurements. Data from regression lines of Wr on Vr and Yr and (Wr+Vr) indicate that lower peak viscosity, lower hot-paste viscosity, lower breakdown viscosity, higher setback viscosity and higher consistency viscosity are dominant and cool viscosity is ambidirectional. However, the degree of dominance for all measurements are incomplete or partial with an exception of peak viscosity in which the complete dominant gene effects is observed. The genetic nature of the parental entries in relation to amylographic viscosity measurements evaluated is discussed in detail.

Key words : Amylographic viscosity measurements, Endosperm characteristics, Diallel graph, Genetic nature.

INTRODUCTION

Amylographic viscosity measurements, a physical property of milled rice flour, and amylose content, a chemical property, are important eating and processing quality parameters[18] and are characteristics of the endosperm, which is a triploid tissue resulting from the fusion of one sperm nucleus with the two ploar nuclei of the egg. Thus, reciprocal differences (including maternal and/or dosage effects, xenia) are supposedly existed. Furthermore, for endosperm characteristics, an individual is a seed, not a plant. That is, these characteristics should be measured on a single grain basis[10]. Unfortunately, there are many endosperm characteristics which are difficult to measure on the basis of a single seed. Thus far, a method for determining amylose content on the basis of a single grain has already been developed[12]. However, determination of amylographic viscosity measurements was not yet developed. Traditional amylographic analysis developed by Halick and Kelly[3]

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and modified for use at the Regional Rice Quality Laboratory, USDA, is based on 50 g of rice flour (grinding about 3000-3500 milled rice grains) in 450 ml distilled water.

Up to the present, a satisfactory quantitative genetic model for such endosperm characteristics has not yet been developed although much attention has been recently devoted to the quality of crop products[10]. Fortunately, according to Hayman[4], when failure of the assumptions has been demondtrated, it is possible to draw the (Wr, Vr) graph and to make estimates of components of variation and other important genetic parameters. Therefore, the diallel cross analysis was used in this experiments. The results presented were based on a bulk sample of seeds which are advanced one generation form the donor plant. For example, F_1 hybrids are represented by bulk F_2 endosperm populations. These flaws mentioned above should be kept in mind.

The regression graph of covariance (Wr, the covariance between these offspring and their non-recurrent parents) and variance (Vr, the variance of all the offspring of the rth parent) of the parent arrays in a diallel cross provides a useful means of assessing genetic relationship among homozygous parents. As Hayman[4], Jana[5], Jinks[6] and Mather and Jinks[9] have shown, the regression graph of Wr on Vr prospectively provides information on four points. First, it supplies a test of the adequacy of the model; in absence of non-allelic interaction and with independent distribution of the genes among the parents Wr is related to Vr by a straight regression line of unit slope. Secondly, given that the model is adequate, a measure of the average level of dominance is provided by the departure from the origin of the point where the regression line cuts the Wr axis. It is partial (incomplete) dominance when the intercept is positive; complete dominance when the regression line passes through the origin, overdominance when the intercept is negative. Thirdly, the relative order of the points along the regression line indicates the distribution of dominant and recessive genes among the parents: the points nearest the origin stem from the arrays derived from parents with most dominant genes and the points furthest from the origin stem from arrays derived from parents with fewest dominant genes. Finally, the remaining information that can be obtained from regression of Wr on Vr is the dirction of the dominance. Comparison of (Wr +Vr) (parental order of dominance) with Yr (parental measurement) indicates whether the distribution of dominant to recessive alleles is correlated with the phenotype of the common parent. The correlation will be negative if the parents with a high score, i.e., those containing most increasing genes, have the lowest values of Wr+Vr, i.e., contain most dominant genes, and positive if the reverse is true. However, if the correlation is non-significant but there is significant dominance, then, dominance is ambidirectional.

In order to further explore the gerntic nature of parental entries used for amylographic viscosity measurements evaluated, genetic analysis by means of diallel graph is presented in this report.

MATERIALS AND METHODS

All possible cross-combinations, including the reciprocals, were made among six rice entries, "Rexmont", "Guichow", "Lemont", "CI 9902", "Toro II", and "Taichung Sen No.

10″ (TCS 10), reprseenting an array of different levels of amylogeaphic viscosity measurements as shown in Fig. 1 and Table 1. The six parents and one set of F_1 hybrids, 30 combinations, were transplanted and cultivated in a flooded paddy field at the Texas A&M University Agricultural Research and Extersion Center near Beaumont, Texas, in a randomized complete block design with three replications. Each block consisted of 36 four-row plots. Each plot included 40 plants spaced at 30×30 cm. Twenty plants from the two central rows of each plot were harvested and analyzed.

Amylographic viscosity measurements were determined by the method devloped by Halick and Kelly[3] and further modified for the use at the Regional Rice Quality Laboratory, USDA, Beaumont, Texas, using a Brabernder Visco/Amylograph with 700 g•cm cartridge and 75 rpm speed (C. W. Brabender Instruments Inc., S Hackensack, NJ). The procedure is outlined as the following. Milled rice sample (about 55-60 g) was ground in a No. 3 Wiley mill equipped with a 0.5 mm screen (do not grind samples more than one day in advance). 50 g of the ground milled rice (12% moisture basis) with 350 ml distilled was blended in a Waring Blender for 1.5 minutes. After blending, the rice-water slurry was rapidly transfrred to the Amylo-Visco-Graph bowl and the transfer was completed quantitatively with an additional 100 ml of distilled water. Thus, the final concentration of the slurry in the Amylograph cup was then 50 g of ground rice in 450 ml distilled water. The Amylogeraph senstivity element was positioned and the thermoregulator was set at 50 °C as the staring temperature. When the temperature reached 50 °C (about 7-8minutes), the chart was adjusted to the zero minute marking and the slurry was then heated to a temperature of 95 °C at a rate of 1.5 °C per minute with the Amylograph control in the "UP" position. When 95 °C was attained (about 30 minutes) the Amylograph control was switched to the "NEUTRAL" position and the paste temperature then was maintained at 95 °C for 10 minutes. After 10minutes of cooking, the cooling solenoid was turned on and the Amylograph control was switched to the "DOWN" position. This permitted paste to cool at a rate 1.5 °C per minute. The curve of amylographic profile was terminated when the paste was cooled to a temperature of 50 °C (about 30 minutes). Significant points in the paste curve are: peak viscosity, hot-paste viscosity (viscosity after cooking at 95 °C for 10 minutes) ; and cool-paste viscosity (viscosity when cooled to 50 °C), all in Brabender Units. Three derivative viscosities, amylographic breakdown, setback, and consistency are calculated from these basic viscosities.

The analytical method is based mainly on Hayman's theory and analysis of diallel crosses[4]. The relative positions of genotypes used with respect to parental measurement (Yr) and parental order of dominance (Wr+Vr) are supplemented with a second graphic treatment based on the standardized deviation of the Yr and the (Wr+Vr), followed by the formula of Johnson and Aksel[7]. Here, the rth array refers to the series of crosses in a diallel in which the rth parent was a recurrent parent. Thus, in this six-parent rice diallel cross experiment, array 1 means that Rexmont (1) is the recurrent parent in all combinations, i.e., 1×1 (parent selfing), 1×2 (Guichow), 1×3 (Lemont), 1×4 (Cl 9902), 1×5 (TCS 10), and 1×6 (Toro 1l).

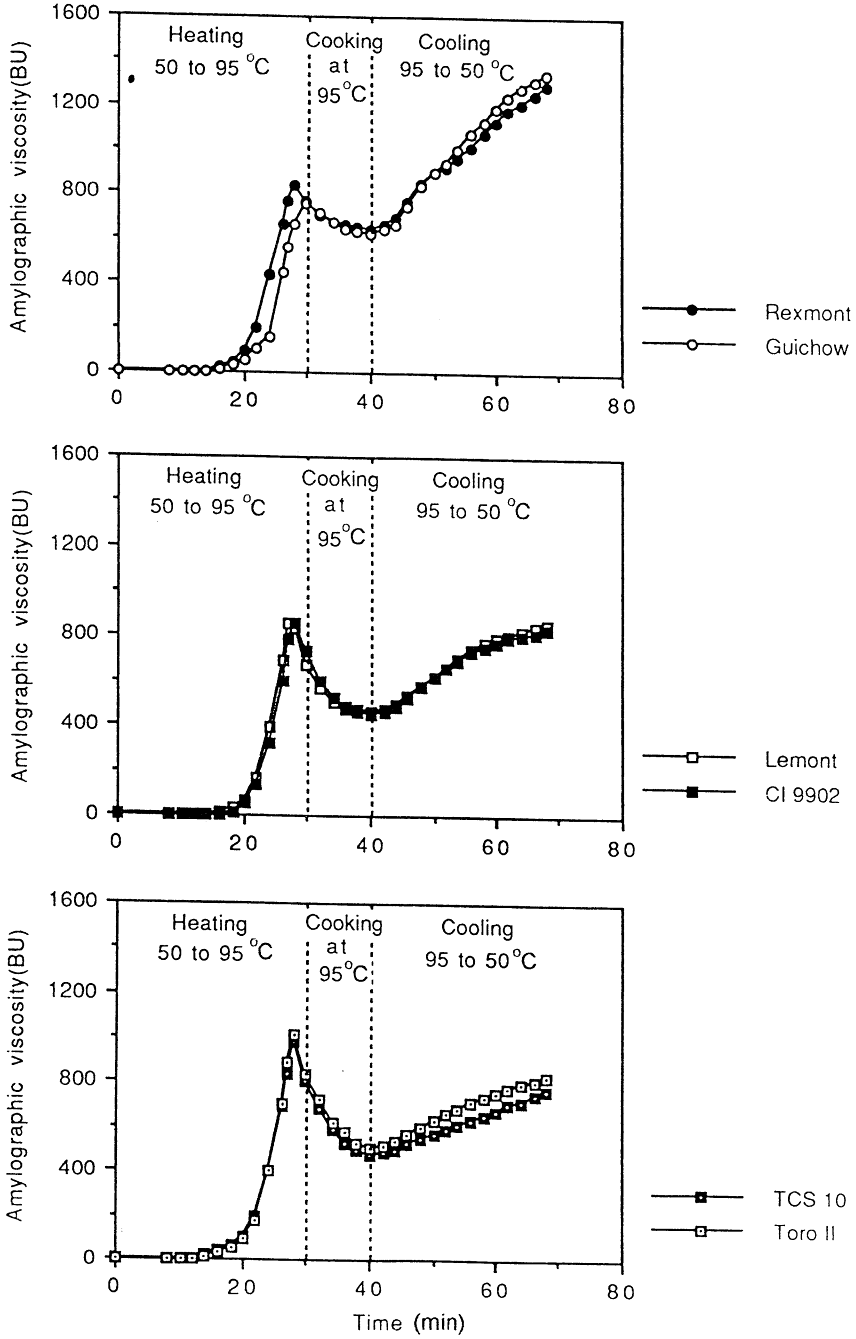

Fig. 1. Amylographic profiles of the six parents used in the diallel cross.

Table 1. Mean values of amylographic viscosity measurements of the six parental entries

Parents	Amylographic viscosity[z]					
	Peak	Hot-paste	Cool-paste	Breakdown	Setback	Consistency
Rexmont(P1)	833	640	1,290	193	457	650
Guichow(P2)	747	620	1,340	127	593	720
Lemont(P3)	843	463	857	380	13	393
CI 9902(P4)	853	470	843	383	−10	373
TCS 10(P5)	997	490	757	507	−240	267
Toro II (P6)	1,010	510	803	500	−207	293

[z] Brabender Unit.

RESULTS AND DISCUSSION

Traditional analyses of variance for viscosity measuremets evaluated revealed highly significant differences among treatments (parents and hybrids) (Table 2), indicating the presence of genotypic variability in these populations used. Further detailed analyses on viscosity measurements were, therefore, performed. The results are presented by individual characteristics as the following.

Table 2. Analysis of variance for amylographic viscosity measurements of rice

SOV	DF	Mean square					
		Peak	Hot-paste	Cool-paste	Breakdown	Setback	Consistency
Block	2	485.5	398.5	156.8	164.2	260.0	65.1
Treatment	35	7,440.7**	2,770.7**	29,283.0**	13,219.4**	54,799.4**	15,347.8**
Error	70	0.26	191.5	90.9	139.4	215.1	98.1

** Significant at the 0.01 probability level.

Amylographic Peak Viscosity

As mentioned above, there are three basic amylographic viscosity measurements: amylographic peak viscosity, amylographic hot-paste viscosity, and amylographic cool-paste viscosity in an amylographic profile. From which, amylographic breakdown viscosity, amylographic setback viscosity, and amylographic consistency viscosity can be calculated. Amylographic peak viscosity is the viscosity when a aqueous suspension of starch of a given concentration is heated. Peak viscosity usually occurs before of after the temperature of the suspension has reached to 92-95 °C. Amylographic peak viscosity is a measurement of the ability of the known starch granules to swell markedly before rupturing. Typical U. S. long-grain rice cultivars usually show an intermediate peak viscosity(13,15,16,17). Scientists in Japan (11) and in Taiwan, ROC.(8) found sticky cooked rice has higher peak viscosity. Thus, amylographic peak viscosity is an important index for evaluating rice grain quality.

The graphic analysis of data on amylotraphic peak viscosity of milled rice flour from the

six-parent rice diallel cross is given in Fig. 2. The regression line, Wr (the covariance between these offspring and their non-recurrent parents) on Vr (the variance of all the offspring of the rth parent), is significantly different from zero and does not differ significantly from the unit slope. The excellent unit-slope linearity demonstrates validity of the assumptions on which the method is based: an additive-dominance model with independence of the genes in action and in distribution. The regression line nearly passes through the point of the origin, indicating an almost complete dominance. However, this result could be due to complete dominance masked by bulking. The positions of the array points (Vr, Wr) along the regression line revealing the relative proportions of dominant and recessive genes in the parents are: Toro II having predominantly recessive genes; Rexmont, Guichow, Lemont, and CI 9902 forming a group in which dominant genes predominate. However, the position of array 2, Guichow, is slightly deviated from the regression line, indicating that little genetic interaction might exist in this parent-array[7].

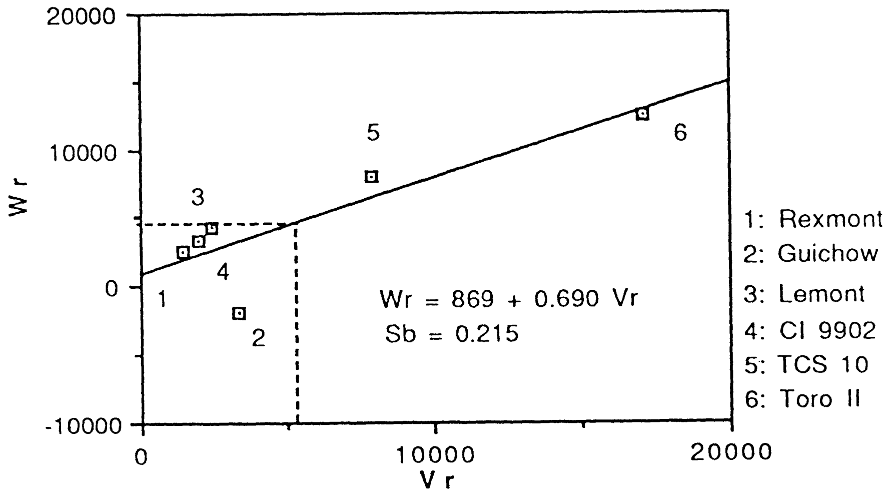

Fig. 2. Regression of Wr on Vr for amylographic peak viscosity in the six-parent diallel cross, dotted lines showing the means of Wr and Vr of arrays, respectively.

The theory of the diallel cross states that the parental measurement (Yr) is closely correlated with the number of positive (increasing) homozygotes in the parent while (Wr +Vr) bears the same relationship to the number of recessive homozygotes. The recessive (decreasing) genes are mostly positive when the correlation coefficient (r) between Yr and (Wr+Vr) is significantly positve. The dominant genes are positive (increasing) when r is significantly negative; When the r is non-significant the equal proportions of the dominant genes are negative (decreasing) and positive (increasing), i.e., ambidirectional dominanec. In the present study, the correlation between Yr and (Wr+Vr) for amylographic peak viscosity shows a marked linearity with a highly significantly positive correlation coefficient

(r=0.92**) between Yr and (Wr+Vr) indicates that high amylographic peak viscosity is associated with recessiveness, and low amylographic peak viscosity is associated with dominance.

Up to this point, the results inferred from the regression graph of Wr on Vr have indicated some basic genetic information about the parents used. The relative positions of entries used with respect to parental measurement (Yr) and the parental order of dominance (Wr+Vr) were further graphically surveyed (Fig. 3). As shown in Fig. 3, recessiveness (+) is shown by points above the horizontal line (parental measuremant) and dominance (−) is shown by points below this line. High parental measurement (+) is shown by points to the right of the vertical line (Wr+Vr) and low parental measurement is shown by points left of this line. Thus, TCS 10 and Toro II, located in the first quadrant, with a predominantly recessive genes produce a relatively high amylographic peak viscosity. Rexmont, Guichow, Lemont, and CI 9902, on the other hand, in the third quadrant, with maximum numger of dominant genes produce a relatively low amylographic peak viscosity. However, Guichow, possessing slightly more dominant genes than those of Rexmont, Lemont and CI 9902, show a relative low amylographic peak viscosity.

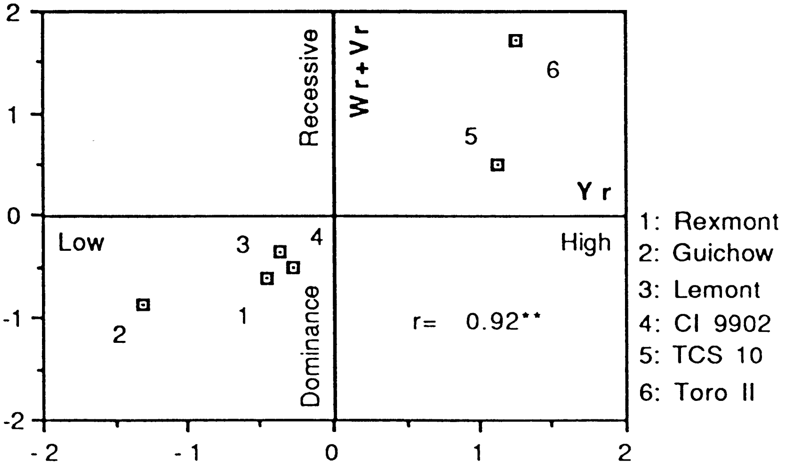

Fig. 3. Standardized deviation for amylographic peak viscosity in the six-parent diallel cross, showing parental measurement (Yr) and parental order of dominance (Wr+Vr) .

Amylographic Hot-Paste Viscosity

Amylographic hot-paste viscosity is measured as the paste is cooking at a specified high temperature (usually 92-95 °C) for 10 minutes. The overall relationship between amylographic hot-paste viscosity and grain quality is not clear, although Lii et al.[8] reported that amylographic hot-paste viscosity significantly positively correlated with eating quality.

The graphical analysis of data on amylographic hot-paste viscosity form the six-parent rice diallel cross is illustrated in Fig. 4. The regression line is significantly different from

zero and does not differ significantly from unit slope as shown in Fig. 4. Thus, the excellent unit-slope linearity demonstrates adequacy of an additive-dominance model with independence of the genes in action and in distribution. The regression line crosses the Wr axis fairly high above the point of the origin, indicating a small degree of dominance, i.e., a slightly partial or incomplete dominance. However, this result could also be due to complete dominance masked by bulking.

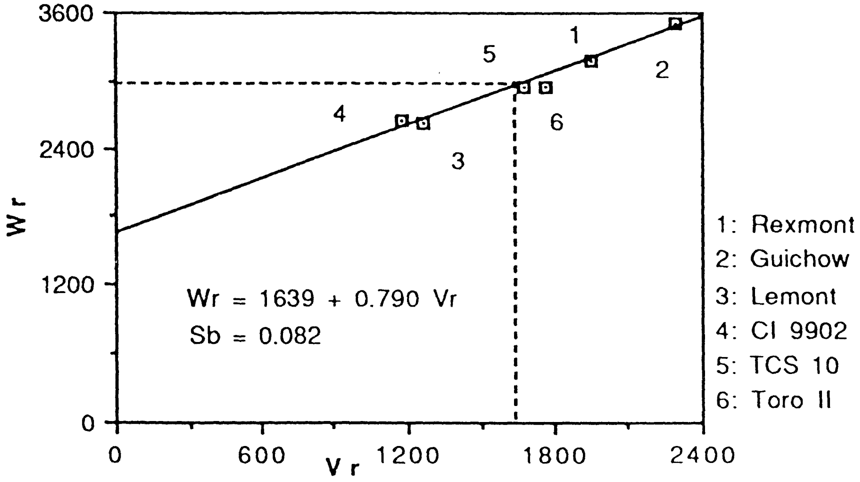

Fig. 4. Regression of Wr on Vr for amylographic hot-paste viscosity in the six-parent diallel cross, dotted lines showing the means of Wr and Vr of arrays, respectively.

The positions of all arrays are near the regression line, confirming very little genetic interaction. However, all arrays closely correspond to the points distant from the lower ends of the line. Guichow and Rexmont have, in that order, mostly recessive genes; Lemont and CI 9902 have, also in that order, more dominant genes; TCS 10 and Toro II have, on the other hand, recessive and dominant genes in nearly equal proportions as indicated by the fact that these two paraental arrays are located near the point which is intersected by the lines of the means of Wr and Vr of arays, especially TCS 10.

The standardized deviation graph of Yr and (Wr+Vr) were plotted (Fig. 5). As presented in Fig. 5, a significant correlation coefficient ($r=0.82^*$) between parental measurements and parental order of dominance indicates that the association of lower amylographic hot-paste viscosity with dominance and of higher amylographic hot-paste viscosity with recessiveness is consistent, which reflects the order of dominance observed from Fig. 4. Among all parent arrays, Lemont and CI 9902 with most dominant genes show lower values for amylographic hot-paste viscosity; Rexmont and Guichow possessing mostly recessive genes produce relatively high values for amylographic hot-paste viscosity.

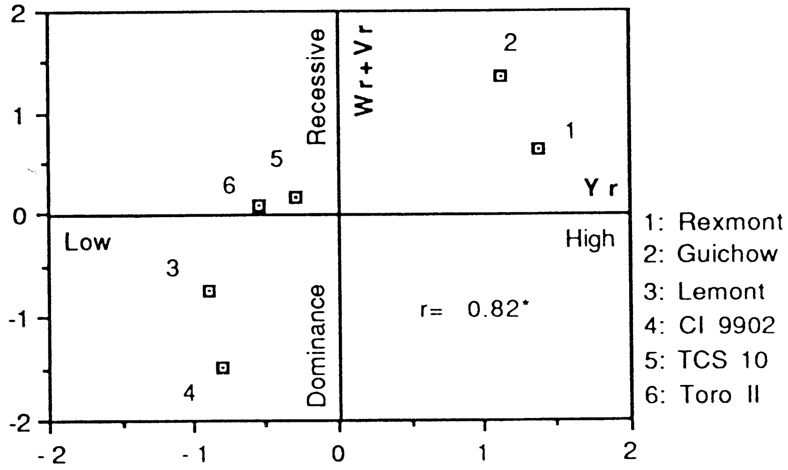

Fig. 5. Standardized deviation for amylographic hot-paste viscosity in the six-parent diallel cross, showing parental measurement (Yr) and parental order of dominance (Wr+Vr).

Amylographic Cool-Paste Viscosity

Amylographic cool-paste viscosity is measured as the temperature of the paste is cooled down at a certain rate (usually 1.5°C/min.) to 50°C after a holding period (usually 10 minutes) at a specified high temperature (usually 92—95°C). Typical U. S. medium-and short-grain cultivars show a comparatively low cool-paste viscosity[13,15,16,17]. However, a higher amylographic cool-paste viscosity combined with lower amylographic breakdown viscosity has been correlted with superior parboil-canning characteristics and quick-cooking properties[18]

Data on amylographic cool-paste viscosity for the six-parent rice diallel cross were analyzed graphically (Fig. 6). The regression coefficient differs significantly form zero but not from unity, demonstrating validity of the assumptions on which the analysis is based. The regression line intersects the Wr axis significantly above the point of the origin, proposing a small degree of dominance among the arrays, i.e., partial or incomplete dominance. However, this result could also be due to complete dominance masked by bulking.

The arrays form two groups: TCS 10 and Toro II having, in that order, the maximum number of recessive genes; Rexmont, Guichow, Lemont, and CI 9902 forming a group in which dominant genes predominate. However, the position of this dominant group is near the intersection of the means of Wr and Vr of the arrays and far from the point of the origin, indicatig that these parents contain only slightly more dominant genes than recessive genes. Also, all group are positioned close to the regression line, indicating very little genetic interaction.

The correlation between parental measurement and parental order of dominance is a non-significant negative correlation (r=−0.69ns), indicating that equal proportions of the

dominant genes are positive (increasing) and negative (decreasing), i.e. ambidirectional dominance. This was further illustrated by the relative positions of parent-arrays plotted in Fig. 7. TCS 10 and Toro II, as shown in Fig. 7, with the most recessive genes, have a relatively lower amylographic cool-paste viscosity. In contrast, the dominant parental group can be divided into two groups: Rexmont and Guichow with some dominant genes show a relatively high amylographic cool-paste viscosity; on the other hand, Lemont and CI 9902 also with equal amount of dominant genes compared to Rexmont and Guichow show a relatively low amylographic cool-paste viscosity. The fact that equal proportions of dominant genes are positive (increasing) and negative (decreasing) can be confirmed form the observations made in Fig.6. and Table 1.

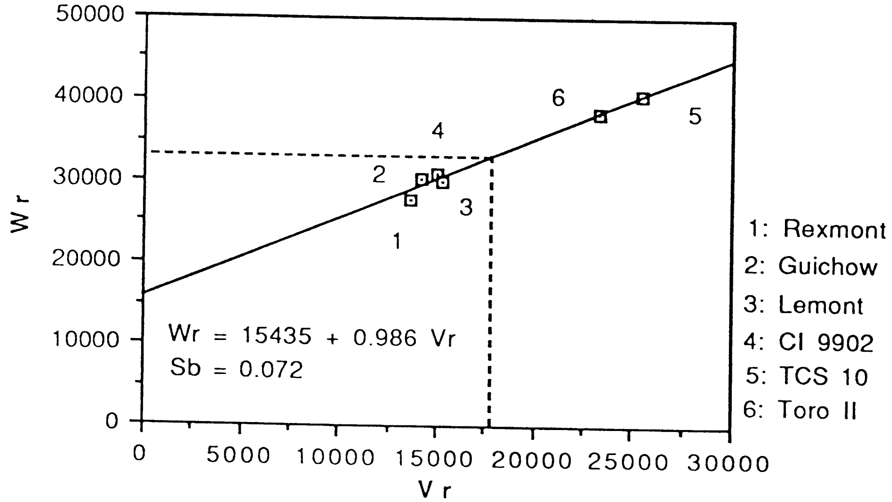

Fig. 6. Regression of Wr on Vr for amylographic cool-paste viscosity in the six-parent diallel cross, dotted lines showing the means of Wr and Vr of arrays, respectively.

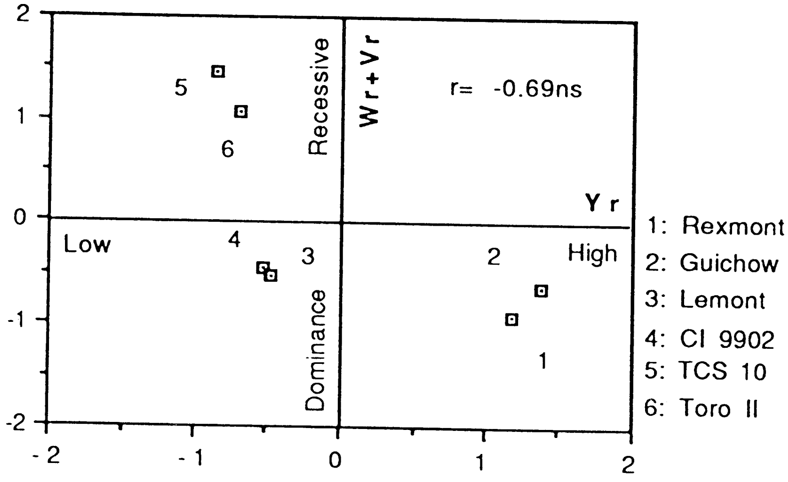

Fig. 7. Standardized deviation for amylographic cool-paste viscosity in the six-parent diallel cross, showing parental measurement (Yr) and parental order of dominance (Wr+Vr).

Amylographic Breakdown Viscosity

There are three derivative amylographic viscosity measurements: amylographic breakdown viscosity, amylographic setback viscosity, and amylographic consistency viscosity. Amylographic breakdown viscosity is calculated from amylographic peak viscosity minus amylographic hot-paste viscosity and reflects the decrease in viscosity during cooking at 92—95°C.

Traditional U. S. long-, medium-, and short-grain cultivars show relatively high amylographic breakdown viscosity. In contrast, superior cooking and processing U. S. long-grain cultivars are characterized by an amylose content 2—4% higher than those of typical U. S. long-grain cultivars and a relatively low amylographic breakdown viscosity(1,2,14,16,18). A low breakdown viscosity is indicative of lower loss of solids and little splitting and fraying of edges and ends in canning(18). On the other hand, Japanese rice scientists suggested that amylographic breakdown viscosity could be selected as an index factor for palatability evaluation(11). Published results from Taiwan, ROC. suggested a highly significant correlation between amylographic breakdown viscosity and eating quality(8). Amylographic breakdown viscosity, therefore, could be considered as the most important index for evaluating grain quality among all of the six amylographic viscosity measurements.

The regression line, illustrated in Fig. 8, is significantly different from zero at the 1% probability level, and is not significant different from unity, indicating an additive-dominance model without the complication of gene interatcion. The regrassion line crosses the Wr axis slightly above the point of the origin, suggesting a moderate degree of dominance among the arrays. Therefore, partial or incomplete dominance is involved in conditioning amylographic breakdown viscosity. However, this result could also be due to complete dominance masked by bulking.

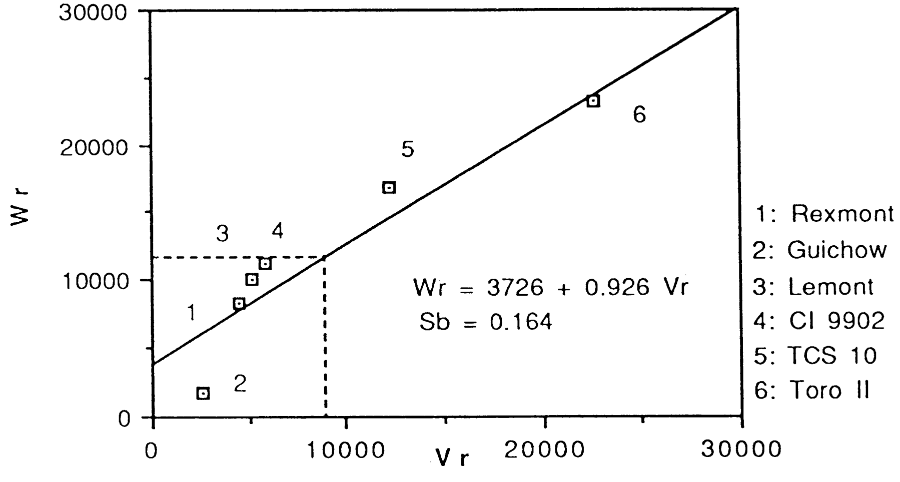

Fig. 8. Regression of Wr on Vr for amylographic breakdown viscosity in the six-parent diallel cross, dotted lines showing the means of Wr and Vr of arrays, respectively.

The order of the parental arrays along the regression line indicating the relative proportions of dominant and recessive genes among the parents are: Toro II possessing most recessive genes, and Guichow, the parent bearing the most dominant genes. Furthermore, the position of Guichw is slightly form the regression line, indicating little gene interaction might exist[7].

Standardized deviation graph of parental measurement (Yr) and parental order of dominance (Wr+Vr) were plotted (Fig. 9). The correlation coefficient is significant at the 5 % probability level (r=0.84*), suggesting an association between recessive and high amylographic breakdown viscosity and between dominance and low amylographic breakdown viscosity. The genetic nature of amylographic breakdown viscosity of the parents used is: TCS 10 and Toro II possessing most recessive genes and showing a relatively high amylographic breakdown viscosity; Rexmont and Guichow containing most dominant genes and having a relatively low amylographic breakdown viscosity; Lemont and CI 9902 with few dominant genes producing an intermediate amylographic breakdown viscosity.

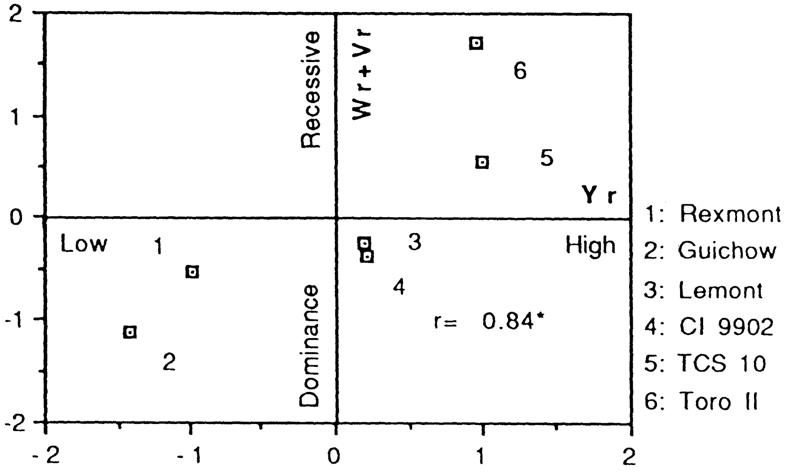

Fig. 9. Standardized deviation for amylographic breakdown viscosity in the six-parent diallel cross, showing parental measurement (Yr) and parental order of dominance (Wr+Vr).

Amylographic Setback Viscosity

Amylographic setback viscosity is a derivative amylographic viscosity measurement calculated from amylographic cool-paste viscosity minus amylographic peak viscosity. Traditional southern U. S. long-grain cultivars show a slightly positive amylographic setback viscosity. Superior cooking andr Processing U. S. long-grain cultivars, on the other hand, show a higher amylographic sethack viscosity[1,2,14,16,18]. Thus, amylographic setback

viscosity is also an important index for evaluating grain quality although more attention has traditionally been paid to amylose content and amylographic breakdown viscosity.

The graphic analysis of amylographic setback viscosity is presented in Fig. 10. The regression line, Wr on Vr, is significantly different from zero and does not differ significantly from unit slope, demonstrating an additive-dominance model without the complication of gene interaction. The regression line cuts the Wr axis slightly above the point of the origin, indicating a small degree of dominance. However, this result could also be due to complete dominance masked by bulking, The positions for all arrays are near to the regression line. Toro II and TCS 10 have, in that order, predominantly recessive genes. Rexmont, Guichow, Lemont, and CI 9902 from a dominant gene group. Among this group, Guichow possesses the maximum number of dominant genes.

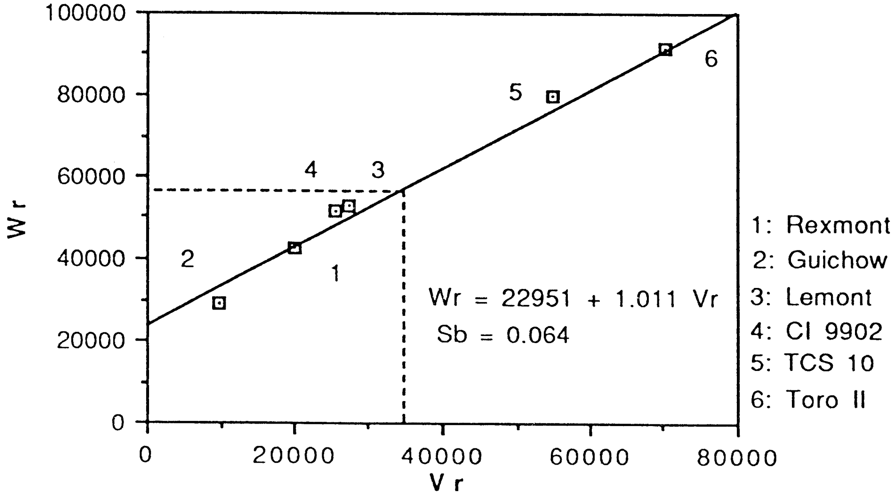

Fig. 10. Regression of Wr on Vr for amylographic setback viscosity in the six-parent diallel cross, dotted lines showing the means of Wr and Vr of arrays, respectively.

The standardized deviation graph for parental measurements and parental orders of dominance, given in Fig. 11, shows a marked linearity with a significant correlation, r = − 0.88*. The association of low amylographic setback viscosity with recessiveness and of high amylographic setback viscosity with dominance is consistent in Fig. 11. Among these parent arrays, TCS 10 and Toro II with the most recessive genes show a relatively low amylographic setback viscosity; Rexmont and Guichow, higher amylographic setback viscosity parents, possess mostly dominant genes; Lemont and CI 9902, intermediate setback viscosity arrays, contain a slight excess of dominant genes.

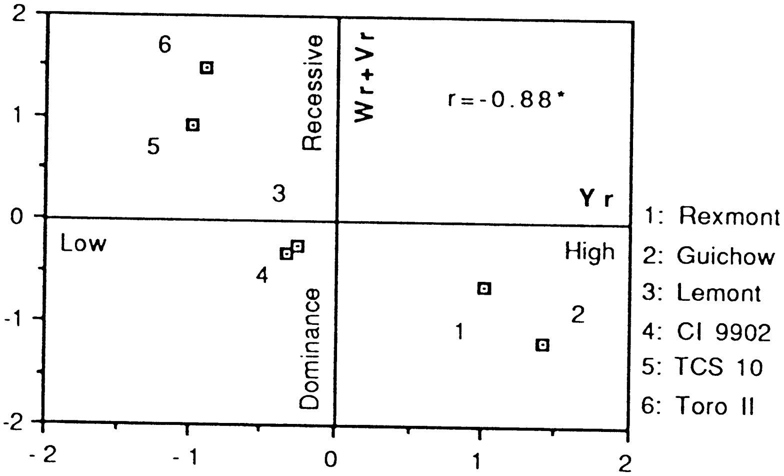

Fig. 11. Standardized deviation for amylographic setback viscosity in the six-parent diallel cross, showing parental measurement (Yr) and parental order of dominance (Wr+Vr).

Amylographic Consistency Viscosity

Amylographic consistency viscosity is one of the derivative amylographic viscosity measurements calculated by subtracting amylographic hot-paste viscosity form amylographic cool-paste viscosity. Up to now, less attention has been paid to this measurement.

The graphic analysis of data on amylographic consistency viscosity is illustrated in Fig. 12. The regression coefficient is significantly different from zero, but not from unit slope, verifying the validity of the assumptions on which the analysis is based. The regression line intersects the Wr axis significantly above the point of the orgin, indicating a small degree of dominance among these parent arrays. However, this result could also be due to complete dominance masked by bulking.

From the positions of the arrays along the regression line, it is apparent that TCS 10 and Toro II both contain, in that order, the greatest number of recessive genes. Rexmont, Guichow, Lemont, and CI 9902 form a dominant gene group. However, Rexmont and Guichow possess more dominant genes than those of Lemont and Cl 9902.

The graph of standardized deviation of parental measurements and parental order of dominance for this characteristic is presented in Fig. 13. The correlation coefficient between these variables is significant at the 5% probability level (r=−0.86*), suggesting an association between low amylographic consistency viscosity and recessiveness, and between high amylographic consistency viscosity and dominance. Thus, Rexmont and Guichow possessing the maximum number of dominant genes show a high amylographic consistency viscosity; TCS 10 and Toro II contaning the greatest amount of recessive genes produce a low amylographic consistency viscosity.

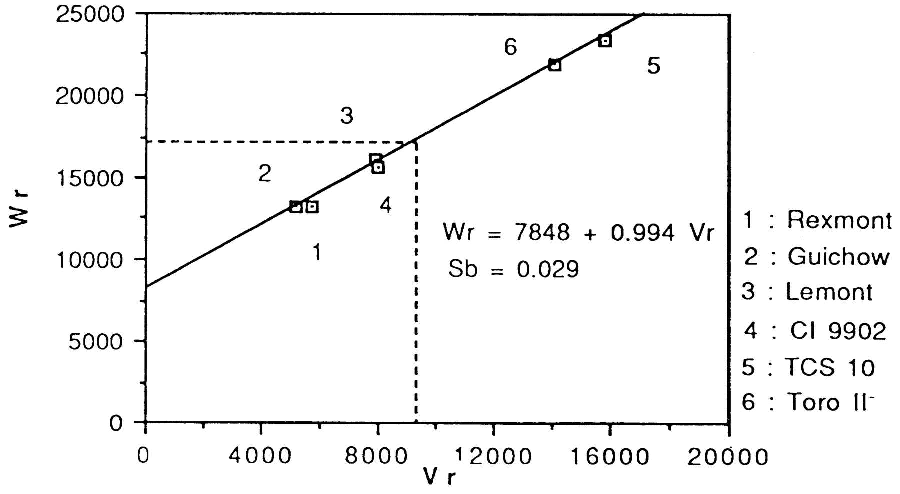

Fig. 12. Regression of Wr on Vr for amylographic consistency viscosity in the six-parent diallel cross, dotted lines showing the means of Wr and Vr of arrays, respectively.

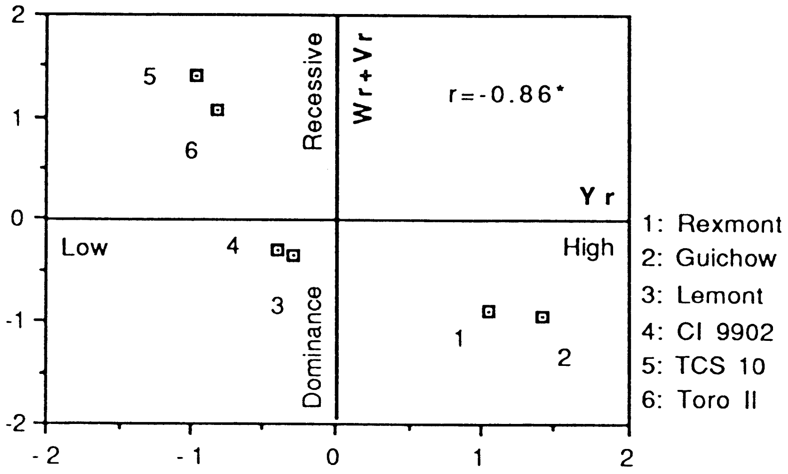

Fig. 13. Standardized deviation for amylographic consistency viscosity in the six-parent diallel cross, showing parental measurement (Yr) and parental order of dominance (Wr+Vr).

From the results presented above, it might concisely conclude that effective selection for targeted viscosity measurements can be easily done from the crosses between the parental entries used because of an additive-dominance model with independence of the genes in action and in distribution is demonstrated by the excellent unit-slope linearity for all viscosity measurements.

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白米澱粉糊黏度測定值之全互交遺傳圖析[1]

郭益全[2] 偉伯比爾[3] 史譚索詹姆士[4]

摘 要

白米澱粉糊黏度測定值是稻米食用與加工品質非常重要之介量，屬胚乳性狀。本研究利用全互交遺傳圖析進行白米澱粉糊黏度測定值之遺傳分析。由各黏度測定值良佳之迴歸斜率線性獲證：基因作用與分布獨立之累加性一顯性遺傳模式適用於這些被評估之黏度測定值。圖析顯示：低高峰黏度、低熱糊黏度、低崩解黏度、高回饋黏度及高膠質黏度爲相對顯性；冷糊黏度爲雙向顯性。除高峰黏度爲完全顯性外，各該黏度測定值概呈不完全或部份顯性。文中曾就參試親本澱粉糊度測定值之遺傳特質詳細討論。

關鍵詞：澱粉糊黏度測定值、胚乳性狀、全互交遺傳圖析、遺傳特質。

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區域試驗不均衡資料之穩定性子集合分析[1]

呂　秀　英[2]

摘要：本省區域試驗一般採用的穩定性介量多以最受廣泛使用的直線迴歸分析法爲主。該法僅適用於每一基因型與環境組合都有資料之場合，因此一旦含有缺區，便無法正確估得環境指標，並進行穩定性分析；過去一般處理缺區的方式，係將含缺區的品系或環境全部刪除，使其呈均衡資料後，再進行穩定性分析，如此在缺區數多時勢必會造成品系或環境數減少，反而降低了評估結果的準確度。對此，本研究利用子集合分析法以擴大穩定性分析之應用範圍至不均衡的區域試驗資料。子集合分析可處理含交感模式之不均衡資料，在觀念上相當簡單直接，係就所分割成的兩個不同子集合均衡資料各進行穩定性分析，並利用兩子集合重疊部份，對共存環境下之品系進行穩定性選拔。惟該法在使用上必須注意，所有品系的共存環境數不得太少。

關鍵詞：子集合分析、穩定性、區域試驗、不均衡資料、迴歸。

育種程序中區域試驗施行之目的，在選出高產且穩定之品種。本省區域試驗一般採用的穩定性介量多以最受廣泛使用的直線迴歸分析法爲主，即必須對每一基因型以各環境所有重複之平均性狀觀測值隨環境指標（environmental index）作迴歸。目前大部份的穩定性分析法僅能適用於每一基因型與環境組合都有資料之場合，尤其是直線迴歸分析模式，因此一旦含有缺區，便無法正確估得環境指標，並進行穩定性分析；至於每一基因型與環境組合都有資料，但重複不等，因爲仍然是以其重複平均值進行迴歸分析，故無影響，在此並不將之視爲區域試驗穩定性分析的缺區現象。過去一般處理缺區的方式，係將含缺區的品系或環境全部刪除，使其呈均衡資料後，再進行穩定性分析，如此在多量缺區的情況下勢必會犧牲不少辛苦調查收集之試驗資料，而且一旦欲刪除的品系爲重要品系或環境數原本即少的情形下，尤其可惜，同時也因爲品系或環境數減少，反而降低了評估結果的準確度。對此呂[2]曾考慮在不摒除任何品系及環境數之情況下，利用傳統的缺區估計法使填入缺區估計值後，以均衡資料的型態再進行標準穩定性分析，結果發現，雖然缺區估計法相當簡單，但因爲會造成缺區品系之穩定性係數低估，故僅適用於穩定品系含少數一、二個缺區的場合，一旦缺區發生在不穩定品系時，容易使原來不穩定品系被誤認爲是穩定。這是由於以無交感模式來預估實際上交感顯著存在的區域試驗資料之缺區值，是不恰當的，故並不適用於試驗中含有對環境反應較敏感的不穩定品種[2]。至於其他以填入估計值進行缺區矯正的程序，例如常數配合法（fitting constant method）[9,14,18,21]，因爲也是用以分析處理組合因子間無交感效應時的複因子試驗不均衡資料，仍會使得穩定性分析的結果產生偏誤[5]。

基本上，針對部份缺區之統計方法，可廣泛地分爲以下幾種類別，而彼此間互不排斥[12,13]：㈠放棄不均衡記錄單位而僅就均衡的部份資料進行分析（complete-case analysis）；㈡利用有用之最

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大資料集合來估計個別介量的方法（available-case methods）；㈢填入估計值使呈均衡資料後以標準方法分析的程序（imputation-based procedures）；㈣加權的程序（weighting procedures）；㈤以定義一缺區資料之模式爲基礎的程序（model-based procedures）。第一類方法最爲簡單，但會損失所拋棄之不均衡資料的相關訊息。上述所提之缺區估計屬於第三類。至於第四類則涉及較繁複的統計理論及計算程序，而且效率亦有待質疑，例如將加權值引入迴歸分析模式中，利用迭代接近法（iterative method）求得穩定性迴歸估值時，必須注意迭代接近法可能有無法收斂的問題[5]。第五類程序中以常數配合法及最大可能估計法（maximum likelihood estimation）爲最常見的方法；常數配合法係假設在一個複因子試驗無交感效應存在之約束模式（restricted model）下僅分析主效應的方法，不適用於含交感效應的情形[5]；而將缺區視爲介量以求均衡資料之最大可能函數的方法，雖然有其優點[11]，但僅在某些特殊場合有效，且一般引用於不均衡資料之分析並不普遍可靠，除非樣品大小增加到缺區所佔比例已近於0時，否則該法並不能獲致適當的性質[12]。因此，本研究主要針對第二類的缺區處理策略在區域試驗不均衡資料之適用性進行探討。在不摒除現有品系及環境之原則下，子集合分析（subset analysis）或許是第二類中可以考慮採用的方法之一，藉此以擴大穩定性分析之應用範圍至不均衡的基因型與環境組合資料。

統計方法

一、穩定性迴歸分析法

將基因型 i（i=1,…,m）在環境 j（j=1,…,n，爲地區與年度之組合）下的平均性狀觀測資料 y_{ij} 以下列數學模式表之：

$$y_{ij}=\mu+G_i+E_j+I_{ij}+e_{ij} \qquad [1]$$

式中

$\hat{\mu}$＝總平均值＝$\sum_{i=1}^{m}\sum_{j=1}^{n}y_{ij}/mn=\bar{y}_{..}$

$\hat{G}_i$＝基因型 i 的遺傳效應＝$\bar{y}_{i.}-\bar{y}_{..}$，而 $\bar{y}_{i.}=\sum_{j=1}^{n}y_{ij}/n$

$\hat{E}_j$＝環境 j 的效應＝$\bar{y}_{.j}-\bar{y}_{..}$，而 $\bar{y}_{.j}=\sum_{i=1}^{m}y_{ij}/m$

$\hat{I}_{ij}$＝基因型 i 與環境 j 之交感效應＝$y_{ij}-\bar{y}_{i.}-\bar{y}_{.j}+\bar{y}_{..}$

e_{ij}＝試驗機差，而符合平均值爲 0，變方爲σ^2之常態分布。

並假定：

$\sum_{i=1}^{m}G_i=0$，$\sum_{j=1}^{n}E_j=0$，$\sum_{i=1}^{m}I_{ij}=\sum_{j=1}^{n}I_{ij}=0$，亦即假定 G_i，E_j 及 I_{ij} 均爲固定型效應[20]。

由於交感效應多呈環境指標的直線函數，

$$I_{ij}=\beta_i E_j+\theta_{ij} \qquad [2]$$

故直線迴歸模式可寫成

$$y_{ij}=\mu+G_i+E_j+\beta_i E_j+\theta_{ij}+e_{ij} \qquad [3]^{(15)}$$

$$=\mu+G_i+(1+\beta_i)E_j+\theta_{ij}+e_{ij} \qquad [4]^{(8)}$$

$$=a_i+b_i E_j+\theta'_{ij} \qquad [5]^{(6)}$$

式中 θ_{ij} 爲離迴歸機差，$a_i=\bar{y}_{i.}$，b_i 爲各基因型平均性狀觀測值隨環境指標作迴歸所得的迴歸係數，一般皆以最小平方法（LS）來估計。農業育種學家多以 b_i 定義爲基因型 i 的穩定性係數（stability index）[6,8]：b=1 爲合乎一般農業要求的穩定基因型，其表現在有利環境下可獲改善，但處

於不利時也不致於太差；0≦b<1 爲符合生物觀點之穩定性，該類基因型之表現在優勢中也許不十分傑出，但在劣勢裡可保持相當的忍耐力；b>1 則爲不穩定或可塑的基因型，其對環境之變異相當敏感，環境之改善固然可獲致最大的增進，但環境變壞，其表現亦差。至於選取何者爲選拔準則，端視實際需要而決定。倘以 G×E 交感效應隨環境指標作迴歸所得的迴歸係數β而言[15]，則相當於以$\beta=-1$或$\beta=0$來選拔出符合生物或農業觀點的穩定品系。

二、子集合分析

子集合分析是專門用來處理不均衡資料中模式有交感的其中一種統計方法，又稱爲格均值分析（cell means analysis）。在變方分析（analysis of variance）中，若觀測值被安排在雙向配置（two-way layout）之表格內時，其安放之位置形如格子狀，爲最小之試驗單位，則稱此一方格爲「格」。在變方分析中，每一格內之觀測值所取的平均值，謂爲格均值。複因子試驗中各格（或稱各處理組合）之觀測值數相等的資料，稱爲均衡資料；若各格之觀測值數不等，稱爲不均衡資料。不均衡資料中至少有兩類特殊情形，係屬於均衡資料之標準分析範圍內，即規劃上之不均衡性及缺區，前者例如拉丁方設計、均衡不完全區集試驗等，後者爲資料及規劃上皆形同均衡，但僅少數觀測值缺失之情況。眞正不均衡資料係摒除以上兩種不均衡性外，爲格內觀測值數不相等（含很多格內無觀測值）的情形，而又可分爲兩類：所有格填滿的資料，以及某些空格的資料。各種類別的不均衡資料，可根據因子間交感效應存在與否，各有不同的適應分析方法：當所有格填滿資料時，交感模式以均值加權平方法（weighted squares of mean analysis）或格均值分析進行，而無交感模式則只行主效應分析；若是某些爲空格的資料且模式有交感時，僅能使用格均值分析[17]。

區域試驗實際上是一個含有品種及地區兩因子的複因子試驗，其線性模式中並含有基因型與環境之交感效應，因此觀測值 Y 在 m－n 單位（假設有 m 品種 n 環境）上的缺區現象，應該視爲含交感之某些空格的不均衡資料，故可以採用格均值分析中的子集合分析。

所謂子集合分析，就是將 m－n 單位（m×n 兩向表）的不均衡資料集分割成均衡的資料集，這兩個資料集各爲原來資料集的一個子集合，然後再就各子集合分別進行統計分析與結果解釋。事實上，這些子集合資料的分析因互有重疊，故並不互相獨立，但分析上顯然變得極爲簡單，而且個別之解釋上也很直接。

材料及方法

本研究利用呂及曾[1]之飼料玉米綜合新品系區域試驗資料爲分析材料，以檢視本研究所擬方法的適用性。試驗於1986年春作至1987年秋作進行，計二年四期作。參試品系包括 PC8、PC7、PCC、PUC 及對照品系（CK）之臺南選10號，分別於臺東縣東河鄉、臺東縣鹿野鄉及花蓮縣萬榮鄉共 3 個地區進行試驗。新品系 PC8 及 PC7 均爲自國際玉米小麥研究中心（International Maize and Wheat Improvement Center, CIMMYT）引進之抗倒伏的熱帶型半硬粒種，PCC 及 PUC 則爲本省朴子分場培育之熱帶型硬粒重。各試驗之田間設計採用逢機完全區集法（RCBD），四重複，按當地高級產量試驗標準，六行區，行長 5m，行株距 75×25cm，小區面積 22.5m²，田間作業管理採一般方式執行，調查公頃籽實產量（kg/ha）。

區域試驗所調查的產量結果及環境指標估值列於表 1。本研究之玉米區域試驗係以地區及年度之組合作爲環境變異，故合計 5 個品系 6 個環境進行穩定性分析。爲方便說明，並使一目瞭然，以下相關圖表及其說明將簡化符號，設品系代號各爲 V1～V5，而環境代號各爲 E1～E6。不均衡資料組則是利用人爲的方式，刪去該 5 × 6 兩向表資料中的一個或一個以上的單位（格）資料，使造成缺區現象。爲探討缺區發生在穩定或不穩定品種時，其對各種理論分析所造成的可能影響，因此根據均衡資料的穩定性分析結果，分別就表現出不同穩定度（穩定性係數 b<1、b=1、b>1）的品種，逢機

刪去部份資料，以模擬成各種含有缺區的不均衡資料組。這些不均衡資料組均將利用子集合分析，先將其分割成兩個均衡的子集合後，再就各子集合分別進行標準的穩定性迴歸分析，利用兩子集合資料互有重疊之部份，對所有參試品系在共存環境下的綜合表現作一整合性的推論，以選出理想的優良品種。

表1. 春作五個玉米品系於六個環境（兩年×三地區）下生長的四重複平均籽實產量資料（公斤／公頃）

Table 1. Mean kernel yield (kg/ha) of four replicates on five maize varieties grown in six environments (2 years×3 sites) under spring crop season

Variety	Environment[y]					
	E1	E2	E3	E4	E5	E6
V1 (PC8)	3,289	2,163	3,692	3,921	1,589	1,805
V2 (PC7)	3,487	1,660	3,148	3,897	1,937	1,404
V3 (PCC)	2,651	1,996	2,375	2,920	982	1,158
V4 (PUC)	2,467	2,095	2,575	3,743	1,846	1,489
V5 (CK)[z]	2,753	1,761	3,913	4,179	1,890	1,678
Average	2,929	1,935	3,141	3,732	1,649	1,507
Envir. index	447	−547	659	1,250	−833	−975

[z] CK：臺南選10號 (Tainan sel. No. 10)
[y] E1：1986臺東縣東河鄉 (Tongho, Taitung)
E2：1986臺東縣鹿野鄉 (Louyai, Taitung)
E3：1986花蓮縣萬榮鄉 (Wanlong, Hualien)
E4：1987臺東縣東河鄉 (Tongho, Taitung)
E5：1987臺東縣鹿野鄉 (Louyai, Taitung)
E6：1987花蓮縣萬榮鄉 (Wanlong, Hualien)

結　果

一、原始均衡資料的穩定性分析結果

本研究飼料玉米綜合新品系區域試驗以均衡資料進行之綜合變方分析結果列於表 2，品系與環境之交感效應呈極顯著，顯示參試品系間對環境的反應不一致，其穩定性分析的結果，如表 3 所示。由表 3 得知，各品系的分析結果均滿足直線迴歸法應用於穩定性分析的兩個重要統計前提，即各品系之迴歸係數 (b) 均顯著存在（直線關係成立），同時所有品系之迴歸離差均方 (S^2d) 不顯著且互爲均質，因此所求得之迴歸係數估值 (b) 足以解釋基因型對環境之適應能力。各參試品系之 b 值間的差異未達0.05之顯著水準，但如需進一步再互作比較，四個新品系的 b 值均相對地較臺南選10號之對照品系 (CK) 爲低，即表現可更爲穩定，其中 PC8 及 PC7 之 b 值最接近於1，爲符合農業觀念之穩定品種，其會隨著環境改善而表現增進，但也不致因爲環境不利而表現太差，PCC 及 PUC 之 b 值爲0.81，小於1，對環境的變異亦相當穩定，尤其在惡劣環境下可較 PC8 及 PC7 穩定，但因環境改善所能提高的產量卻不如 PC8 或 PC7 高，爲符合生物觀念的穩定性；對照品系 (CK) 的 b 值大於1，表示其穩定性相對地較其他四個新育成品系爲低。由於育種上欲選拔優良的品系，須兼顧穩定性及生產力，故一般均同時以穩定性介量與產量平均值爲選拔依據，如表 3 所示，如以優於對照品系爲選拔之目標，而 PC8 應爲最理想的優良品系，其有較高的產量及穩定性。

表2. 玉米品系春作籽實產量區域試驗之綜合變方分析結果

Table 2. Combined analysis of variance for kernel yield of maize varieties in a regional trial under spring crop season

Source	D. F.	Mean squares
Block/Environment	18	125,359.5
Environment (E)	5	16,057,406.8**
Variety (V)	4	2,241,246.5**
V×E	20	458,425.3**
Error	71	174,205.0

** significant at 1% level.

表3. 玉米品系春作籽實產量區域試驗以直線迴歸法進行穩定性分析之結果

Table 3. Stability analysis of kernel yield of maize varieties in a regional trial under spring crop season using linear regression method

Variety	Mean yield (a)	Stability index (b)	Deviation from regression (S^2d)
V1 (PC8)	2,743 a[z]	1.10**	41,876
V2 (PC7)	2,589 ab	1.11**	96,429
V3 (PCC)	2,014 c	0.81**	107,299
V4 (PUC)	2,369 b	0.81**	92,001
V5 (CK)	2,695 a	1.17**	136,976
Average	2,482	1.00	94,917
LSD (0.05)	237	0.31	
Bartlett's χ^2			1.25[ns]

[z] Means with the same letter of a column are not significantly different at 5% level by LSD Test.
** significant at 1% level under hypothesis b=0.
[ns] nonsignificant at 5% level.

二、不均衡資料的子集合穩定性分析

(一)單一缺區之場合

首先考慮只有一個缺區的最簡單場合，即只有某一環境缺少一個品系。缺區發生處，依上述玉米區域試驗均衡資料之穩定性分析結果，假設其可能是發生在符合生物穩定（b<1）、農業穩定（b=1）或不穩定（b>1）品種的某個環境上。選定這三種不同穩定度的玉米參試品系，分別爲 V1（PC8）、V3（PCC）及 V5（CK）。至於是在哪一個環境缺失資料，則於六個環境中逢機決定。因此所模擬成的單一缺區之三種規劃情形，如圖 1 所示，圖中格內✓符號表示有資料，空白則代表無資料。利用子集合分析，將原來 5 × 6 兩向表之不均衡資料集分割成兩個 5 × 5 及 4 × 6 的子集合，其中第一個 5 × 5 子集合爲包含所有品系但刪去含缺區環境的均衡資料集，而第二個 4 × 6 子集合爲包含所有環境但刪去含缺區品系的均衡資料集。然後再就各子集合分別進行穩定性分析，其所估得的環境指標、產量平均值、穩定性係數及迴歸離差均方的估計值，分別列於表 4 及表 5。

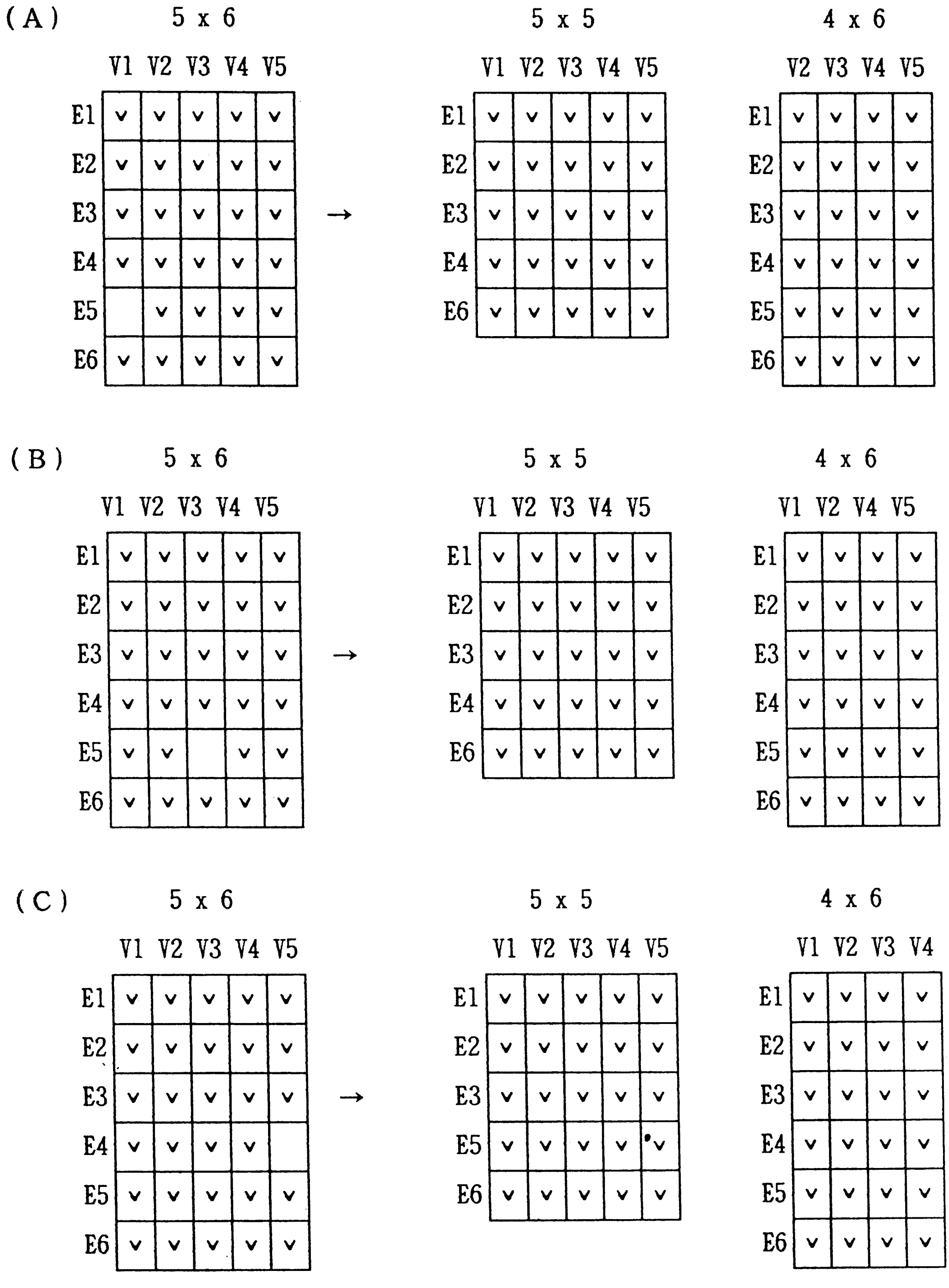

圖1. 玉米區域試驗不同品系含單一缺區時的不均衡資料之子集合分析
(缺區各為A：y_{15}，B：y_{35}，C：y_{54})

Fig. 1. Subset analysis of unbalanced data with only one missing plot occurred on different varieties in a maize regional trial.
(Missing plot occurred on A:y_{15}, B:y_{35}, C:y_{54})

表4. 玉米區域試驗單一缺區之不均衡資料各子集合的環境指標估值

Table 4. Estimates of environmental index for individual subset of unbalanced data with only one missing plot in a maize regional trial

Envir.	V1[z] I[y] 5×5	V1 II 4×6	V3 I 5×5	V3 II 4×6	V5 I 5×5	V5 II 4×6
E1	281	423	281	400	697	545
E2	−714	−539	−714	−679	−297	−450
E3	492	586	492	733	909	519
E4	1,083	1,268	1,083	1,336		1,192
E5		−753		−784	−583	−840
E6	−1,142	−985	−1,142	−1,005	−725	−965
Max.	1,083	1,268	1,083	1,336	909	1,192
Min.	−1,142	−983	−1,142	−1,005	−725	−965
Range	2,225	2,253	2,225	2,341	1,634	2,157

[z] genotype with missing plot.
[y] subset of data.

表5. 玉米區域試驗單一缺區之不均衡資料各子集合的產量平均值、迴歸離差均方及穩定性係數之估值

Table 5. Estimates of mean yield, deviation from regression and stability indices for individual subset of unbalanced data with only one missing plot in a maize regional trial

Variety	V1[z] I[y] 5×5	V1 II 4×6	V3 I 5×5	V3 II 4×6	V5 I 5×5	V5 II 4×6
	Mean yield (a)					
V1 (PC8)	2,974 a		2,974 a	2,743 a	2,508 a	2,743 a
V2 (PC7)	2,719 b	2,589 a	2,719 b	2,589 ab	2,327 ab	2,589 ab
V3 (PCC)	2,220 d	2,014 c	2,220 d		1,833 c	2,014 c
V4 (PUC)	2,474 c	2,369 b	2,474 c	2,369 b	2,094 b	2,369 b
V5 (CK)	2,857 ab	2,695 ab	2,857 ab	2,695 a	2,399 a	
Average	2,649	2,417	2,649	2,599	2,232	2,429
	Deviation from regression (S^2d)					
V1 (PC8)	26,631		26,631	59,757	29,060	58,923
V2 (PC7)	90,369	87,436	90,369	93,519	123,418	88,016
V3 (PCC)	79,876	117,530	79,876		134,581	70,599
V4 (PUC)	111,535	72,593	111,535	93,023	24,985	92,702
V5 (CK)	167,920	147,003	167,920	88,946	182,410	
Average	95,266	106,141	95,266	83,766	98,891	77,560
Bartlett's χ^2	2.83 [ns]	0.54 [ns]	2.83 [ns]	0.23 [ns]	5.30 [ns]	0.24 [ns]
	Stability index (b)					
V1 (PC8)	1.02		1.02	1.04	1.22	1.13
V2 (PC7)	1.20	1.14	1.20	1.06	1.17	1.16
V3 (PCC)	0.70	0.82		0.70	0.88	0.87
V4 (PUC)	0.85	0.84	0.85	0.77	0.56	0.84
V5 (CK)	1.22	1.20	1.22	1.14	1.16	

[z] genotype with missing plot.
[y] subset of data.
[ns] nonsignificant at 5% level.

由於穩定性係一種相對比較的概念，因此可就該兩個不同子集合的穩定性分析結果，予以個別解釋但綜合討論。換言之，吾人可以由第一個 5 × 5 子集合之分析結果，檢視出所有五個品系在其中五個環境下的穩定性表現，而由第二個 4 × 6 子集合之分析結果，比較其中四個品系在所有六個環境下的穩定性表現，由於這些子集合資料的分析互有重疊，即互不獨立，因此進一步可以利用重疊部份，對所有品系在共存環境下的綜合表現作一整合性的推論，以選出理想的優良品種。

由表 4 得知，不同子集合的環境指標估值，除了 V5 於環境 E4 有缺區之場合其兩個子集合的環境變異互有差異以外，其他兩子集合間的環境變異範圍皆頗爲接近。由表 5 得知，無論缺區發生何處，各子集合的產量平均值皆表現一致，產量由高至低，依次爲 V1、V5、V2、V4、V3。各子集合內所有品系之間的迴歸離差均方，皆呈均質，表示符合穩定性直線迴歸模式的統計前提，故所求得之穩定性介量的估計值應足以代表基因型對環境之適應能力（表 5）。由表 5 之穩定性係數估值得知，穩定的 V1（PC8）品系在環境 E5 發生單一缺區時，從子集合 I 的穩定性分析結果發現，在不計環境 E5 的情形下，V1 品系確爲一符合農業穩定的品種（b＝1），V3 及 V4 爲符合生物穩定性的品系（b<1），V2 及 V5 爲不穩定品系（b>1）；而從子集合 II 的穩定性分析結果，V3、V4 及V5 在所有六個環境下的穩定性表現與子集合 I 所獲結果一致，但 V2 的 b 值在加入環境 E5 後而有變小的趨勢，此將使得 V2 變得較爲穩定；綜合兩子集合之分析結果，可推知在不考慮環境 E5 下，所有參試品系中仍應以 V1 爲最符合農業穩定的品系，其次可考慮 V2，至於 V3 及 V4 爲符合生物穩定的品種，V5 則爲最不穩定品種。倘若缺區是發生在符合生物穩定的 V3（PCC）品系時，就兩子集合之穩定性分析分開個別解釋並綜合討論的結果，亦與前述缺區品系爲 V1 之情形所獲品種穩定性評價的結果完全相同。一旦缺區是發生在不穩定的品系（V5），從子集合 I 的穩定性分析結果發現，在不計環境 E4 的情形下，V1 之穩定性最差，在加入環境 E4 後，從子集合 II 的穩定性分析結果來看，V1 的穩定度可獲提高，至於 V2、V3 及 V4 的穩定性則維持不變；綜合兩子集合穩定性分析結果，倘不計環境 E4 下，應選擇 V3 爲最符合農業穩定的品種，因其 b 值最接近於 1，若僅就其中四個品系於所有六個環境之相對性比較，以 V1 及 V3 的穩定性較佳，但此時因缺乏了對照品系（V5），致使育種上優良品種選拔之意義降低。

按品系在重疊部份結果上的差異，則是因爲兩子集合之間的環境變異有較大的不同所致，例如前述之 V5 在環境 E4 有缺區的情形下，V1 在兩子集合間的穩定性分析結果之所以有差異（表 5），可從表 4 之各子集合的環境指標值得到解釋及說明；由表 4 得知，是否加入環境 E4，對環境變異的影響很大，致使子集合 I 的環境變異範圍甚小於子集合 II，又因爲環境 E4 之環境指標估值最大（表 1），爲一最高產環境，對於像 V1 這種實際上符合農業穩定性的品種而言，由於其會隨著環境改善而表現增進，故對高產環境的敏感度更甚於其他品系，因此所受到的影響也較大。至於品系在其他環境有缺區的情形，例如表 5 中之 V1 或 V3 於環境 E5 有缺區之場合，由於 E5 之環境指標爲負值（表 1），即爲一低產環境，但並非爲最低產（並非最大負值），加入與否對環境變異範圍影響不大，故各品系在重疊部份的結果大致相同。

㈡多個缺區之場合

進一步探討子集合分析應用於區域試驗資料含多個缺區的適用性。兩個以上的缺區發生處有三種可能：⑴至少兩個以上的環境缺少同一品系，⑵至少兩個以上的環境缺少不同的品系，⑶某一環境缺少兩個以上的品系。首先以兩個缺區的情形爲例說明，如圖 2 所示：情形 A 爲 E4及

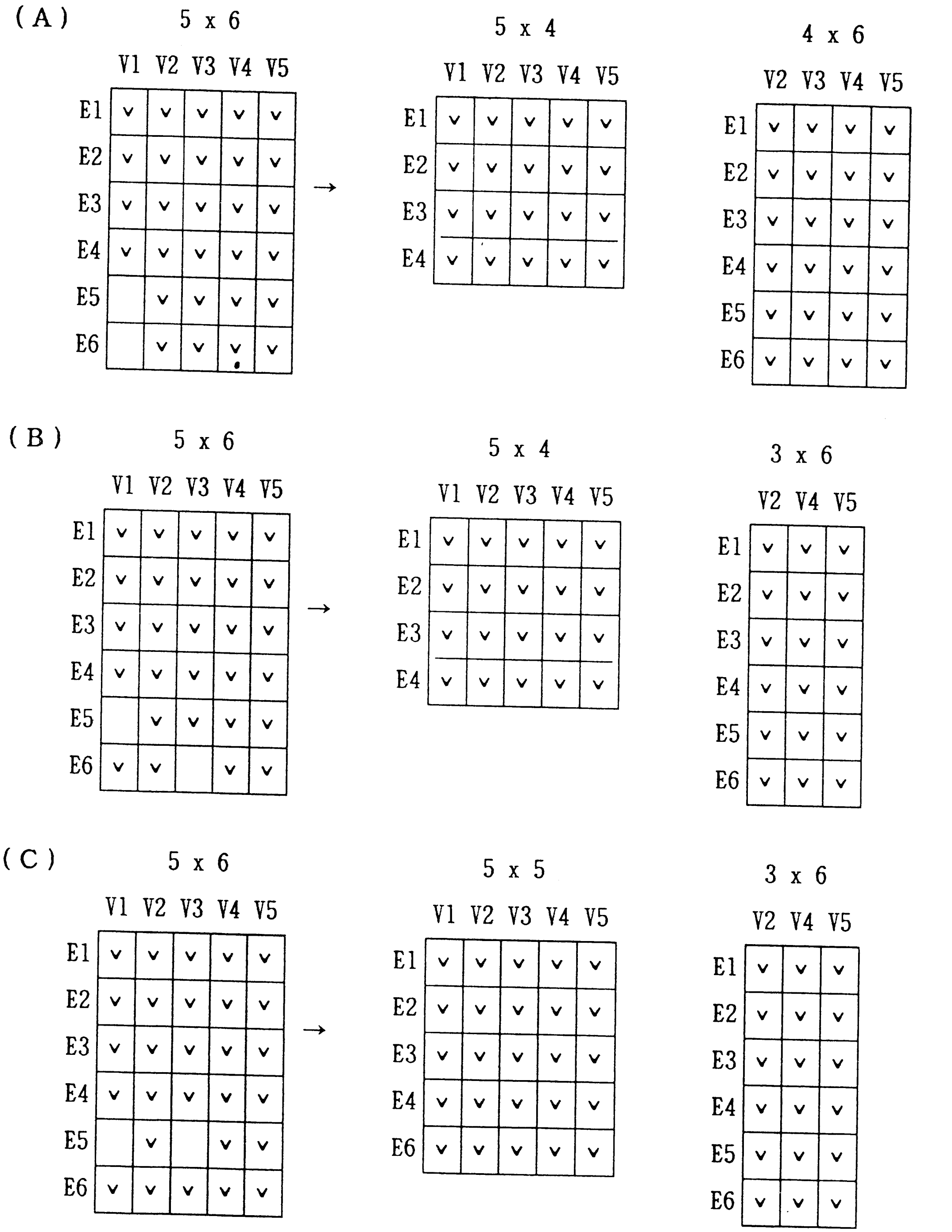

圖2. 玉米區域試驗含兩個缺區時的不均衡資料之子集合分析 (缺區各爲 A:y_{15}, y_{16}; B:y_{15}, y_{36}; C:y_{15}, y_{35})

Fig. 2. Subset analysis of unbalanced data with two missing plots in a maize regional trial. (Missing plot occurred on A:y_{15}, y_{16} B:y_{15}, y_{36}, C:y_{15}, y_{35})

E5 環境均缺少 V1 品系的資料，利用子集合分析可將此不均衡資料分割成兩個 5 × 4 及 4 × 6 的子集合均衡資料集；情形 B 爲 E5 環境缺少 V1 品系且 E6 環境缺少 V3 品系的不均衡資料，子集合分析結果爲兩個 5 × 4 及 3 × 6 的兩個子集合均衡資料集；情形 C 爲 V1 及 V3 品系同時於 E5 環境缺少資料，利用子集合分析將其分割成兩個 5 × 5 及 3 × 6 的子集合均衡資料集，並針對這些子集合個別分開進行穩定性分析。不同子集合的環境指標估值如表 6 所示，其中以含兩個缺區環境的場合（情形 A，B）之兩子集合的環境變異間的差異較大。由表 7 得知，無論缺區發生何處，各子集合的產量平均值均表現一致，產量由高至低，依次爲 V1、V5、V2、V4、V3。各子集合內所有品系之間的迴歸離差均方，皆呈均質，表示符合穩定性直線迴歸模式的統計前提（表 7）。在情形 A 下，倘不計入 E5 及 E6 環境，以 V1 品系爲最符合農業穩定的品種，若於所有六個環境進行選拔，則僅能就 V2、V3、V4、V5 四個品系進行選拔，結果得知 V2、V3、V4 品系之穩定性都略優於 V5，而其中以 V2 最好，其 b 值最接近於 1；在情形 B 下，不計入 E5 及 E6 環境時仍以 V1 品系爲最符合農業穩定的品種，若考慮所有六個環境，則僅能就 V2、V4、V5 品系進行選拔，其中以 V2 最好；在情形 C 下，其結果與其他情形相似，即不考慮缺區環境 E5 時，應選擇 V1品系，如考慮所有環境，則以 V2 品系較其他品系爲優（表 7）。

表6. 玉米區域試驗含兩個缺區之不均衡資料各子集合的環境指標估值

Table 6. Estimates of environmental indices for individual subset of unbalanced data with two missing plots in a maize regional trial

Envir.	Case-A[z]		Case-B		Case-C	
	I[y] 5×4	II 4×6	I 5×4	II 3×6	I 5×5	II 3×6
E1	−5	423	−5	351	281	351
E2	−999	−539	−999	−712	−714	−712
E3	206	586	206	661	492	661
E4	798	1,268	798	1,389	1,083	1,389
E5		−753		−661		−661
E6		−985		−1,028	−1,142	−1,028
Max.	798	1,268	798	1,389	1,083	1,389
Min.	−999	−985	−999	−1,028	−1,142	−1,028
Range	1,797	2,253	1,797	2,417	2,225	2,417

[z] Case-A = missing plots are y_{15}, y_{16}.
Case-B = missing plots are y_{15}, y_{36}.
Case-C = missing plots are y_{15}, y_{35}.
[y] subset of data.

表7. 玉米區域試驗兩個缺區之不均衡資料各子集合的產量平均值 、迴歸離差均方及穩定性係數之估值

Table 7. Estimates of mean yield, deviation from regression and stability indices for individual subset of unbalanced data with two missing plots in a maize regional trial

Variety	Case-A[z]		Case-B		Case-C	
	I[y] 5×5	II 4×6	I 5×5	II 4×6	I 5×5	II 4×6
	Mean yield (a)					
V1 (PC8)	3,266 a		3,266 a		2,974 a	
V2 (PC7)	3,048 a	2,589 ab	3,048 a	2,589 ab	2,719 b	2,589 ab
V3 (PCC)	2,485 b	2,014 c	2,485 b		2,220 d	
V4 (PUC)	2,720 b	2,369 b	2,720 b	2,369 b	2,474 c	2,369 b
V5 (CK)	3,151 a	2,695 a	3,151 a	2,695 a	2,857 ab	2,695 a
Average	2,394	2,417	2,934	2,551	2,649	2,551
	Deviation from regression (S^2d)					
V1 (PC8)	39,945		39,945		26,631	
V2 (PC7)	132,186	87,436	132,186	91,139	90,369	91,139
V3 (PCC)	37,538	117,530	37,538		79,876	
V4 (PUC)	167,119	72,593	167,119	74,311	111,535	74,311
V5 (CK)	192,411	147,003	192,411	96,118	167,920	96,118
Average	113,840	106,141	113,840	87,189	95,266	87,189
Bartlett's x^2	3.99^{n}	0.54^{ns}	3.99^{ns}	0.07^{ns}	2.83^{ns}	0.07^{ns}
	Stability index (b)					
V1 (PC8)	1.02		1.02		1.02	
V2 (PC7)	1.24	1.14	1.24	1.07	1.20	1.07
V3 (PCC)	0.48	0.82	0.48		0.70	
V4 (PUC)	0.84	0.84	0.84	0.79	0.85	0.79
V5 (CK)	1.41	1.20	1.41	1.14	1.22	1.14

[z] Case-A=missing plots are y_{15}, y_{16}.
Case-B=missing plots are y_{15}, y_{36}.
Case-C=missing plots are y_{15}, y_{35}.
[y] subset of data.
[ns] nonsignificant at 5% level.

繼之，再探討子集合分析應用於含三個缺區的區域試驗資料之適用性，仿照上述所提之兩個以上缺區發生的三種可能，列舉如圖 3 所示之三個缺區的五種可能發生情形。這五種缺區發生情形，利用子集合分析可將原來不均衡資料分別分割成兩個子集合之均衡資料，然後再就各子集合個別進行穩定性分析。子集合所含環境數愈少，環境變異範圍愈小，表示這些少數參試環境難以適當地代表整個環境族群（表 8 ）。在考慮所有品系間的產量平均值比較時，仍以 V1 爲最高產的品系（表 9 ）。各子集合均衡資料進行穩定性分析之結果，情形 A、B、D 下在子集合 I 的品系間迴歸離差均方呈異質，即無法符合穩定性直線迴歸模式的統計前提，這是因爲該等子集合所含的環境數太少所致，因此其求得之穩定性係數估值不足以代表基因型對環境之適應能力；換言之，僅有 C、E 之缺區情形，能夠利用子集合分析獲得有效的穩定性評估結果（表 9 ）。在情形 C、E 下，倘不計入缺區環境，由子集合 I 比較所有品系的穩定性表現，可看出應選擇 V1 品系爲最理想的品種，其 b 值最接近於 1 ；但如欲考慮所有環境，則情形 C 只能就 V2、V4、V5 三個品系進行比較，而其中以 V2 較符合農業穩定，但其平均產量低於 V5 之對照品系；至於情形 E 下，倘欲考慮所有環境，則只能就 V4 及 V5 (CK) 進行比較（表 9 ）。

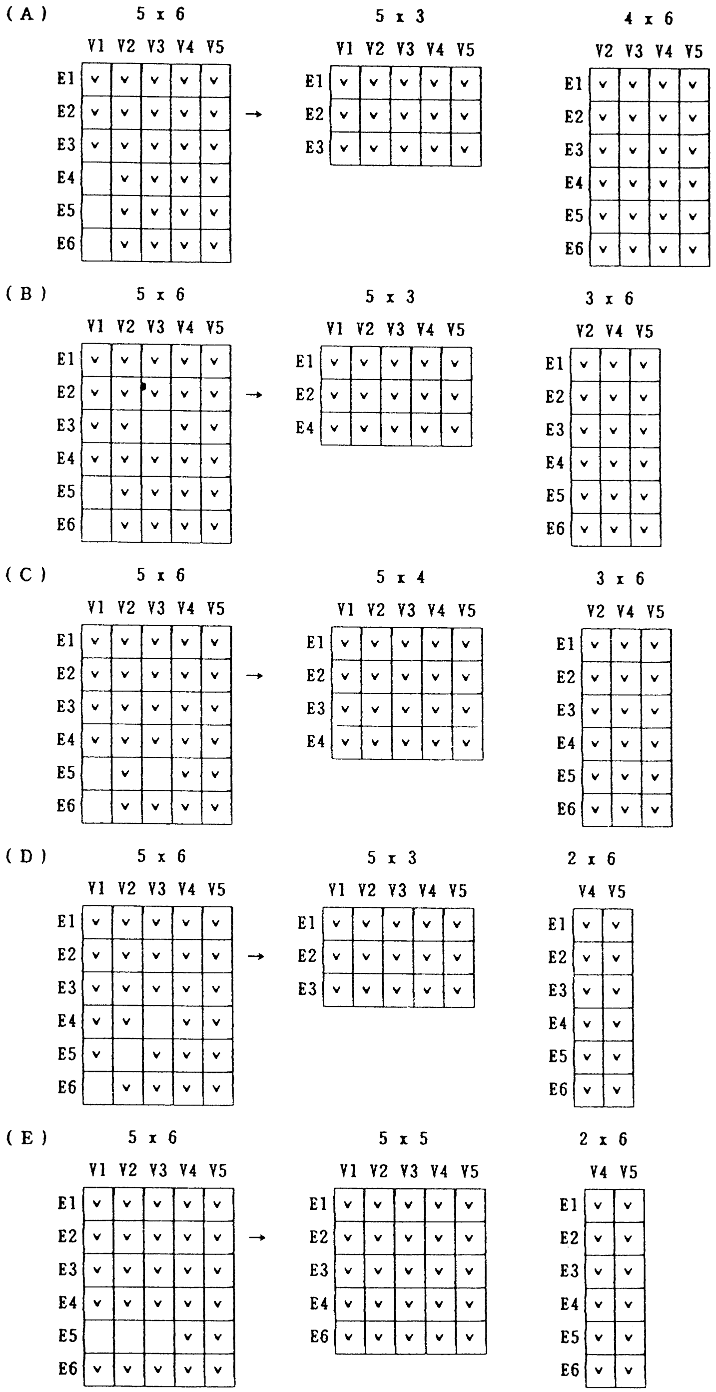

圖3. 玉米區域試驗含三個缺區時的不均衡資料之子集合分析
(缺區各爲 A:y_{14}, y_{15}, y_{16} ; B:y_{15}, y_{16}, y_{33} ; C:y_{15}, y_{16}, y_{35} ;
D:y_{16}, y_{25}, y_{34} ; E:y_{15}, y_{25}, y_{35})

Fig. 3. Subset analysis of unbalanced data with three missing plots in a maize regional trial.
(Missing plots occurred on A:y_{14}, y_{15}, y_{16} ; B:y_{15}, y_{16}, y_{33} ; C:y_{15}, y_{16}, y_{35} ;
D:y_{16}, y_{25}, y_{34} ; E:y_{15}, y_{25}, y_{35})

表8. 玉米區域試驗含三個缺區之不均衡資料各子集合的環境指標估值

Table 8. Estimates of environmental indices for individual subset of unbalanced data with three missing plots in a maize regional trial

Envir.	Case-A[z]		Case-B		Case-C		Case-D		Case-E	
	I[y] 5×3	II 4×6	I 5×3	II 3×6	I 5×4	II 3×6	I 5×3	II 2×6	I 5×5	II 2×6
E1	261	423	64	351	−5	351	261	78	281	78
E2	−733	−539	−930	−712	−999	−712	−733	−604	−714	−604
E3	472	586		661	206	661	472	711	492	711
E4		1,268	867	1,389	798	1,389		1,429	1,083	1,429
E5		−753		−661		−661		−665		−665
E6		−985		−1,028		−1,028		−949	−1,142	−949
Max.	472	1,268	867	1,389	798	1,389	472	1,429	1,083	1,429
Min.	−733	−985	−930	−1,028	−999	−1,028	−733	−949	−1,142	−949
Range	1,205	2,253	1,797	2,417	1,797	2,417	1,205	2,378	2,225	2,378

[z] Case-A = missing plots are y_{14}, y_{15}, y_{16}.
Case-B = missing plots are y_{15}, y_{16}, y_{33}.
Case-C = missing plots are y_{15}, y_{16}, y_{35}.
Case-D = missing plots are y_{16}, y_{25}, y_{34}.
Case-E = missing plots are y_{15}, y_{25}, y_{35}.
[y] subset of data.

表9. 玉米區域試驗含三個缺區之不均衡資料各子集合的產量平均值、迴歸離差均方及穩定性係數之估值

Table 9. Estimates of mean yield, deviation from regression and stability indices for individual subset of unbalanced data with three missing plots in a maize regional trial

Variety	Case-A[z]		Case-B		Case-C		Case-D		Case-E	
	I[y] 5×3	II 4×6	I 5×3	II 3×6	I 5×4	II 3×6	I 5×3	II 2×6	I 5×5	II 2×6
	Mean yield (a)									
V1 (PC8)	3,048 a		3,124 a		3,266 a		3,048 a		2,974 a	
V2 (PC7)	2,765 b	2,589 ab	3,015 ab	2,589 ab	3,048 a	2,589 ab	2,765 b		2,719 b	
V3 (PCC)	2,341 c	2,014 c	2,522 c		2,485 b		2,341 b		2,220 d	
V4 (PUC)	2,379 c	2,369 b	2,768 bc	2,369 b	2,720 b	2,369 b	2,379 c	2,369 b	2,474 c	2,369 b
V5 (CK)	2,809 ab	2,695 a	2,898 ab	2,695 a	3,151 a	2,695 a	2,809 ab	2,695 a	2,857 ab	2,695 a
Average	2,668	2,417	2,865	2,551	2,934	2,551	2,668	2,532	2,649	2,532
	Deviation from regression (S^2d)									
V1 (PC8)	10,798		15,601		39,945		10,798		26,631	
V2 (PC7)	210,264	87,436	230,733	91,139	132,186	91,139	210,264		90,369	
V3 (PCC)	68,765	117,530	13,762		37,538		68,765		79,876	
V4 (PUC)	324	72,593	193,725	74,311	167,119	74,311	324	61,190	111,535	61,190
V5 (CK)	358,635	147,003	79,762	96,118	192,411	96,118	358,635	61,190	167,920	61,190
Average	129,757	106,141	106,717	87,189	113,840	87,189	129,757	61,190	95,266	61,190
Bartlett's x^2	27.69 **	0.54 ns	10.53 *	0.07 ns	3.99 ns	0.07 ns	27.69 **	0 ns	2.83 ns	0 ns
	Stability index (b)									
V1 (PC8)	1.23		0.98		1.02		1.23		1.02	
V2 (PC7)	1.42	1.14	1.27	1.07	1.24	1.07	1.42		1.20	
V3 (PCC)	0.42	0.82	0.52		0.48		0.42		0.70	
V4 (PUC)	0.39	0.84	0.90	0.79	0.84	0.79	0.39	0.81	0.85	0.81
V5 (CK)	1.54	1.20	1.33	1.14	1.41	1.14	1.54	1.19	1.22	1.19

[z] Case-A = missing plots are y_{14}, y_{15}, y_{16}.
Case-B = missing plots are y_{15}, y_{16}, y_{33}.
Case-C = missing plots are y_{15}, y_{16}, y_{35}.
Case-D = missing plots are y_{16}, y_{25}, y_{34}.
Case-E = missing plots are y_{15}, y_{25}, y_{35}.
[y] subset of data.
*,** significant at 5% and 1% level, respectively.
ns nonsignificant at 5% level.

當然，子集合分析也能推至三個以上缺區的場合，但一旦子集合的環境數過少，則進行穩定性迴歸分析的準確度會降低，所得分析結果便不足爲信，因此建議利用子集合分析以處理不均衡區域試驗資料時，在使用上應注意分割後的子集合所含之品系及環境數不得太少，至少要在 3 個以上，才能進行子集合分析。當然，倘若分割後進行穩定性分析的品系及環境數越多，所評估之品系穩定性的結果也越是準確，也才值得信賴。

討　論

綜合上述結果得知，由於子集合分析是使用標準的均衡資料進行統計分析，毋須修正資料及模式即可運用，故在觀念上最爲簡單直接，但必須就所分割成的兩個不同子集合之穩定性分析結果，予以個別解釋，不過由於這些子集合資料的分析互有重疊，故可以進而利用重疊部份，對所有品系在共存環境下的綜合表現作一整合性的推論，以選出理想的優良品種。爲避免因品系及環境數太少而影響穩定性分析之準確度，在使用上應注意子集合所含的品系及環境數，至少要在 3 個以上。另外，利用子集合分析，在拋棄不均衡資料的同時，則有損失訊息的潛在不利點，特別是在含缺區之品系或環境數很多時，樣本大小之損失將相當可觀。某些空格資料以子集合分析進行分析，雖不如均衡資料之變方分析或不均衡但格內均塡滿資料之均值加權平方法可獲致較多的訊息，但效率更高，也較容易了解及解釋，同時也可利用子集合分析來檢視交感效應[17]。有些時候，不均衡資料必須經由兩次以上的分割，始能產生有效的子集合。然而，子集合分析仍可能存在以下困難[17]：(1)並非所有的資料都能被分割成有效的子集合，此時唯一適當的處理方式只能以無交感模式的型態來執行；(2)資料可能被分割成兩種以上完全不同的子集合分析，因此一般而言，某些空格之不均衡資料很少有唯一而確實的統計分析，兩位統計學家可能會對同一套資料有不同方式的分析建議，但並無絕對之對錯，重點端視研究者的興趣在何種比較而已。

導致缺區資料的機制已知或未知，是選擇適當的分析方法及結果解釋的主要因素。由於區域試驗中發生缺區，可能是由於病蟲害、鳥害、機械傷害等因素以致無法收穫，或有記錄但遺失了，或因爲離值被拋棄不用，故其機制在統計上多屬於逢機性型態（missing at random, MAR）[2]，即觀測值 y_{ij} 之缺區可能發生在任一個自變數上，y_{ij} 缺失的機率與，y_{ij} 值無關。在此情況下，可以利用縮減資料之方式使資料呈均衡或近似均衡的型態來分析及敍述，以簡化計算[12]。因此，將子集合分析引用於區域試驗不均衡資料，是可以符合統計理論之要求。反之，倘導致缺區的機制不是樣本選擇之過程，即並非逢機缺失時，該缺區是不可忽略的，此時縮減資料分析是不允許的，因爲會導致估計值偏誤。當區域試驗資料不符合 MAR 時，倘缺區之發生僅與 X 之自變數（環境）有關，傳統的條件推定程序[12,13]只在環境指標能以實際的外在氣候因子來取代時，才能有效地藉由外在環境變數下來推定缺區，此固然有很多優點[3,7,10,16]，但在很多場合，環境的生產水準不可能單純地只由一些有限的環境因子所決定[4]；倘缺區之發生同時與 Y 及 X 有關，即缺區機制爲不可忽略，則爲最難分析的一種，其涉及的問題相當複雜[12,19]。

綜言之，無論是採用何種策略來處理區域試驗缺區的問題，僅利用少數的環境是不可能計算出有效的穩定性估計值。再者，由於迴歸穩定性係數只是提供參試基因型之間的相對等級比較，所以並非一種絕對性的測量值，其所評估的穩定性結果也僅限於該試驗下的環境及品種系統；如果增加極端的環境或品種系統，則穩定性指標會因環境平均值或環境指標平方和之增加（後者會導致迴歸係數之標準機差減少）而改變估計值。此亦說明了利用子集合分析，倘子集合含有極端環境（如本研究之最高產環境），對品系之穩定性評估結果會有差異性的影響。當然，包含的極端環境愈多，交感效應呈非直線的可能性亦增加，此也將使得直線迴歸模式應用於穩定性分析的有效性降低，以致無法解釋基因型對環境之適應能力。

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Subset Method for Assessing Varietal Stability in Unbalanced Regional Trial Data[1]

Hsiu-Ying Lu[2]

Summary

Linear regression analysis is the most common and useful method to assess the varietal stability in a regional trial. However, a major practical limition to date, stability analysis have been a requirement of no missing data, that is, data for every genotype and environment combination or treatment have been necessary. The precison of stability analysis can be unduly influenced by removing all the data of the genotypes or environments which contain missing plot, because of the reduction in number of genotypes and environments. This study proposed a subset method for analyzing stability of unbalanced data in regional trials. Subset analyses for unbalanced data with interaction model were simple and straightforward. The set of unbalanced data was divided into two subsets of balanced data, then one used the stability analysis for these subsets. The analyses of overlapping subsets of the data revealed available information to selecting superior genotypes with common environments. This subset method for stability analysis of unbalanced regional trial data performed well when there were many common environments for genotypes.

Key words : Subset analysis, Stability, Regional trial, Unbalanced data, Regression.

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胡瓜臺農一號之育成[1]

楊偉正　蕭吉雄[2]

摘要：胡瓜臺農一號爲一代雜交品種，其父母本分別爲本省地方品種冬瓜青和臺北育，經八世代自交純化後之固定品系。臺農一號產量穩定，每分地平均產量在4,000公斤左右，早期產量較一般品種爲高。雌花自 4～5 節起開始著生，田間直播至採收，春作和夏作爲44～45天，秋作爲47～49天。果實美觀，品質良好，果實無苦味，果色濃綠，刺白而細少，果皮無網紋或條溝，果心小，果肉較硬，相對失水率低，貯藏性強。臺農一號抗胡瓜嵌紋病毒和木瓜輪點病毒一西瓜系統，中抗矮南瓜黃化嵌紋病毒，白粉病和露菌病。

關鍵詞：胡瓜、育種、臺農一號、一代雜交種。

胡瓜爲本省重要夏季蔬菜之一，根據農業年報記載目前種植面積有3,163公頃，年產量50,544公噸，以高屏地區爲主要產地[2]。胡瓜用途很廣，瓜果可涼拌生食、作菜煮湯、醃漬製罐，汁液具有舒展肌膚，防止臉部皺紋等功效[1,5]。近年來本省胡瓜栽培地區普遍受到病毒病、露菌病、白粉病、疫病、萎凋病、炭疽病和細菌性斑點病等爲害[3,4,10]，尤其是在生長盛期更爲嚴重，影響產量和品質，致使農民收益受損，降低農民栽培意願。作者等有鑑於此，以本系所收集之 8 個地方品種或國外引進品種育成之自交系，進行全互交，獲得28個組合並做組合力檢定，選出12個組合力較佳之雜交組合，進一步進行品系比較試驗，再選出農試183號和132號兩個組合，最後經區域試驗、穩定性測驗及抗病性檢定等試驗，選出產量、品質及抗病性均不遜於對照品種之農試183號組合。於八十三年五月二十四日由臺灣省政府農林廳組成新品種命名審查委員會，經全體委員審查一致通過，准予登記命名爲「臺農一號」，又稱新綠。

材料及方法

一、試驗材料

本試驗使用農發18號、竹山品種、白菜瓜接胡瓜、冬瓜青、雙頭齊、臺北育、萬綠、臺中目瓜等 8 個品種，經多年自交所選育之自交系，其代號、自交系名稱和重要園藝性狀分別詳述如表 1。

1. 臺灣省農業試驗所　研究報告 1870 號。

2. 本所園藝系副研究員及研究員兼系主任。臺灣省　臺中縣　霧峰鄉。

表 1. 供試 8 個胡瓜自交系之代號、自交系名稱和重要園藝性狀
Table 1. Cucumber inbred lines used for the experiment and their horticultural characters

代 號	自交系名稱	園 藝 性 狀
A	農發18號	大瓜、濃綠色、果身平滑
B	竹山品種	大瓜、淺綠色、果身皺溝
C	白菜瓜接胡瓜	大瓜、淺綠色、果身斑紋
D	冬瓜青	大瓜、濃綠色、果身平滑
E	雙頭齊	大瓜、淺綠色、果身斑紋
F	臺北育	大瓜、綠色、果身平滑
G	萬綠	大瓜、濃綠色、果身平滑
H	臺中目瓜	大瓜、綠色、果身平滑

二、試驗方法

(一)全互交及組合力檢定

民國75年進行農發18號等 8 個自交系之全互交（不包括反交及自交）共獲得28個雜交組合，於76年春作在農業試驗所試驗田進行組合力檢定，田間試驗採用逢機完全區集設計，種植行株距爲100×50公分，四重複，每一重複各種20株，四重複共種2,240株。田間栽培管理均依照一般胡瓜栽培方式進行。生育期間調查各種園藝性狀，包括早產量、早果數、總產量、總果數、雄花始花期、雌花始花期、第一朵雌花著生節位、果重、果長、果寬、果肉厚、株高、節間長、側蔓數等項目。試驗結果採用 Griffing 氏[9] Method 4 Model 1 方法，以估算各項園藝性狀的一般及特定組合力。

(二)品系比較試驗

由上項組合力檢定試驗所獲得較優的12個雜交組合，另加對照品種萬綠（F_1），總計13個，採用逢機完全區集設計，行株距100×50公分，四重複，每一重複各種50株，四重複共種2,600株。生育期間調查各種重要園藝性狀及田間自然感病情形。

(三)區域試驗

1. 春作

經品系比較試驗後選出農試183號及132號 2 個品系，於78年春作在雲林縣崙背鄉、臺中縣霧峰鄉；80年春作在雲林縣大埤鄉、臺中縣霧峰鄉；81年春作在雲林縣大埤鄉、屏東縣鹽埔鄉、臺中縣霧峰鄉；82年春作在雲林縣大埤鄉、屏東縣鹽埔鄉、臺中縣霧峰鄉等地，辦理區域試驗，以商業品種萬綠（F_1）和綠豐（F_1）爲對照品種，採逢機完全區集設計，行株距以該地區慣行之行株距爲準，四重複，每重複各種160株，共計2,560株。

2. 秋作

所選之農試183號及132號 2 個品系，同樣於78年秋作在雲林縣崙背鄉、臺中縣霧峰鄉；79年秋作在屏東縣九如鄉、臺中縣霧峰鄉；81年秋作在雲林縣大埤鄉、屏東縣鹽埔鄉、臺中縣霧峰鄉等地，辦理區域試驗，以商業品種萬綠（F_1）和綠豐（F_1）爲對照品種，採逢機完全區集設計，行株距以該地區慣行之行株距爲準，四重複，每重複各種160株，共計2,560株。

(四)產量和果數穩定性

農試183號及132號 2 個品系曾利用其在81年春作及82年春作各 3 點之區域試驗產量成績，以直線迴歸方程配合，求其直線迴歸係數值，以探討在不同地區之產量和果數穩定性[6]。

㈤抗病性檢定

1. 白粉病抗病性檢定

利用感病品種健綠爲接種源，在試驗進行前三週，先行催芽後定植於10吋栽培盆內，俟幼苗生長至本葉5片時，在溫室內以人工接種白粉病病原菌（*Erysiphe cichoracearuum*）使其發病，在發病情況嚴重時做爲試驗中的接種原。臺農一號於第一片本葉展開時，模擬天然條件下病原孢子經由風力四處散佈之情形，採用自然感染方式，將接種原分置於供試品種（系）四周，利用溫室內空氣流動及風扇之抽風作用，將病原孢子散佈於供試植株上，接種二週後進行第一次調查，以後每隔一週調查一次，共調查三次，以三次發病指數之平均值作爲抗病性評估之依據。病害等級係依據葉片上所產生之病斑或菌絲多寡，第 0 級（N_0）爲在肉眼下無病徵出現，第 1 級（N_1）爲僅有 1～4 個小白斑出現，大小在 2～3mm 以下，第 2 級（N_2）爲病斑有擴大能力且數目上亦增多，第 3 級（N_3）爲病斑面積佔了葉片一半以上，並且有孢子產生，第 4 級（N_4）爲葉面大部份爲菌絲覆蓋外，在植株莖部、葉柄部亦受到菌絲爲害，並且產生大量孢子[11]。由發病等級所計算之發病指數，來推斷其感病性，其計算公式如下：

$$\text{發病指數}=\frac{N_0\times 0+N_1\times 1+N_2\times 2+N_3\times 3+N_4\times 4}{N\times 4}\times 100$$

感病性：發病指數在 0～10表極抗，11～20表抗，21～30表中抗，31～40表中感，41～50表感，51～100表極感。

2. 露菌病抗病性檢定

臺農一號經催芽後直播於 4 吋育苗杯，當植株長到 5 片本葉時，利用小型噴霧器接種露菌病病原菌（*Pseudoperonospora cubensis*）孢子懸浮液（4×10^4/ml），然後將接種過之植株置於濕室內，以保持濕度，隔天取出置於網室內，一週後調查其發病情形，調查每一植株由頂部向下之 5 個葉片之發病情形，作爲抗病性評估之依據。病害等級係依據植株本葉病斑發生之多寡，第 0 級（N_0）爲葉片無病斑，第 1 級（N_1）爲葉片有 1～5 個病斑，第 2 級（N_2）爲葉片有 6～15 個病斑，第 3 級（N_3）爲葉片有 16～30 個病斑，第 4 級（N_4）爲葉片有 31 個病斑以上[7]。

$$\text{發病指數}=\frac{\Sigma\ (\text{指數}\times\text{該指數罹病葉片數})}{4\times\text{全部調查葉片數}}\times 100$$

感病性之表示如白粉病。

3. 病毒病抗病性檢定[13]

⑴胡瓜嵌紋病毒（Cucumber mosaic virus）檢定

臺農一號種子經催芽後，直接播種到 4 吋育苗杯裡，俟幼苗長至二片本葉時，開始接種，將已感染病毒之夏南瓜葉片取下，加入10倍量（w/v）之 0.1M，pH＝7.1 之磷酸緩衝液，經研磨過濾後所得之病毒汁液作爲接種原，供試幼苗灑上微量之400目金鋼砂，用研磨棒沾病毒汁液後，磨擦在灑有金鋼砂之子葉和本葉上，接種過之幼苗靜置 2～3 分鐘後，用清水沖洗，再放置溫室內定期調查葉片病徵，作爲抗病性評估之依據。病害等級係依植株葉片之病徵及發病嚴重程度而定，第 0 級（N_0）爲葉片外觀無病徵，第 1 級（N_1）爲葉片有黃色斑點病徵，第 2 級（N_2）爲葉片有斑紋和／或嵌紋病徵，第 3 級（N_3）爲葉片有葉脈綠化和／或嚴重嵌紋病徵，依病徵等級再計算發病指數，其計算公式和感病性之表示如白粉病。

⑵矮南瓜黃化嵌紋病毒（Zucchini yellow mosaic virus）檢定材料與實施步驟如胡瓜嵌紋病毒檢定。

(3)木瓜輪點病毒一西瓜系統（Papaya ringspot virus-type w）檢定材料與實施步驟如胡瓜嵌紋病毒檢定。

(六)果實測定

1. 果實顏色變化之測定

自田間逢機每重複各採收三個胡瓜果實，以奇異筆分別在果實的果梗、腰部和尾部標出直徑約 1cm 的圓圈各三點，一果共 9 點，測量採收後貯放在室溫下一星期之果色變化情形，以色差計（LFM 3 Colorimeter）測 L、a、b 值，L 值表示亮度，a 值表示紅色度（＋a 表示紅色度，－a 表示綠色度），b 值表示黃色度（＋b 表示黃色度，－b 表示藍色度）。

2. 果實失重率之測定

田間逢機每重複各採收三個胡瓜果實放置在室溫下，每一果實於採收後先測最初的重量，隨後每隔二天，分別稱重量的變化，求其重量損失百分率，作成失重變化之曲線圖。

3. 果實硬度變化之測定

田間逢機每重複各採收三個胡瓜果實，以奇異筆分別在果實的果梗、腰部和尾部標出直徑約 1cm 的圓圈各三點，一果共 9 點，測量採收後貯放在室溫下八天間之果實硬度變化情形，以 FHK 果實硬度計，8mm 針頭分別壓入果實有用奇異筆畫圓圈的位置。

(七)主要園藝性狀調查方法

1. 雄花始花期：由播種日起至試區中有50％植株開雄花之日數。
2. 雌花始花期：由播種日起至試區中有50％植株開雌花之日數。
3. 第一朶雌花著生節位：由播種日起至試區中有50％植株開雌花之節位。
4. 產量和果數：由播種後80天內所採收到之果實重量和果實。
5. 早產量和早果數：爲採收期頭 7 天所採收到的果實重量和果實。
6. 株高：每試區逢機選取10株，量自基部起25節之長度平均值，以公分表示之。
7. 側蔓數：上述植株25節內所發生之側蔓平均值，以公分表示之。
8. 果重、果長、果寬：每試區逢機選取20果，調查果實重量、果長和果寬，爲20果之平均值，以公克和公分表示之。
9. 果肉厚：上述果實剖開後，調查果肉厚度，爲20果之平均值，以公分表示之。
10. 果心長和寬：上述果實剖開後，調查果心長與寬，爲20果之平均值，以公分表示之。
11. 果實糖度：上述果實剖開後，測果肉汁液糖度，爲20果實之平均值，以 Brix° 表示之。
12. 果實硬度：每試區逢機取20果，用 FHK 果實硬度計，在果實表面果梗部、腰部及尾部，各取三點測其硬度，爲20果之平均值。

結果與討論

一、全互交及組合力檢定

供試28個雜交組合的產量及其他主要園藝性狀詳見表 2。經評估各組合之總產量、早產量、第一朶雄花始花期、第一朶雌花始花期和著生節位、植株生長勢、果實品質、果重、果色、果形外觀等性狀，選出12個雜交組合分別爲 A×B＝農試524號，A×C＝農試338號，A×D＝農試123號，B×D＝農試178號，B×E＝農試425號，B×H＝農試127號，C×E＝農試124號，C×F＝農試128號，C×G＝農試129號，D×F＝農試183號，D×G＝農試132號，E×G＝農試130號，這12個組合不僅總產量和早產量較其他組合爲高，其餘各主要園藝性狀如果數、果重、果寬，植株高度等性狀均比28個雜交組合之平均值爲高，生長勢、果實色澤、果實外觀亦較其他組合好，然而第一朶雌花始花期和著生節位卻比28個雜交組合之平均值爲低，這表示第一朶雌花始花期較早，著生節位較低。

表 2. 28個全互交組合之產量及重要園藝特性平均值（76年秋作）

Table 2. Mean yield and horticultural characters of 28 dialle-cross combinations in fall crop 1987

供試組合	產 量 (kg)	早產量 (kg)	果 數 (條)	早果數 (條)	第一朵雄花開花日數	第一朵雌花開花日數	第一朵雌花開花節位數
A × B[z]	51.0e[y]	21.0d-f	68.5b-i	25.0b-e	39.4ab	42.6a-e	7.7d-h
A × C	47.3b-e	21.3d-f	65.8a-g	27.5e-f	39.2a	41.2a	7.4c-g
A × D	48.5de	20.1c-g	65.5a-g	24.0a-e	39.9a-d	43.8e	8.1e-i
A × E	46.0b-e	23.0ef	62.3a-f	26.3b-e	40.0a-e	45.7i	8.7h
A × F	45.5b-e	19.0b-g	62.5a-f	22.8a-e	39.7a-d	44.4e	8.4fj
A × G	40.3ab	16.8a-d	60.3a-d	22.5a-e	39.3ab	45.4h	8.6g
A × H	33.5a	12.4a	61.0a-e	23.5a-e	40.5d	41.7a-d	4.2a
B × C	46.0b-e	17.8a-e	58.0a	20.5a-c	39.9a-d	43.3b-g	7.6d-h
B × D	50.6e	18.7b-g	69.3c-i	24.0b-e	40.4c	42.9a-f	6.7b-d
B × E	50.0e	22.0d-g	69.8d-i	26.8b-f	39.8a-d	43.3b-e	8.0d-e
B × F	40.2ab	14.5ab	59.0a-c	16.5ab	40.0a-e	45.2g	7.2c-f
B × G	40.5a-c	12.7a	58.8ab	16.3a	39.7a-d	45.5h	7.2c-f
B × H	50.6e	17.7a-e	73.8g	22.3a-e	40.0a-e	42.5a-e	6.7b-d
C × D	46.5b-e	16.4a-d	65.5a-g	21.5a-d	40.9e	44.7fj	7.0a-e
C × E	49.2de	20.0b-g	67.0a-h	25.3b-e	39.5a-c	44.8f	8.8a-e
C × F	49.6e	18.9b-g	72.3f	26.8b-f	39.6a-d	44.3e	8.7h
C × G	48.4de	23.6fg	72.0f	34.0fg	39.4ab	41.5ab	6.7b-d
C × H	41.7bc	14.7a-c	69.3c-i	24.5b-e	40.2b	42.9a-f	7.0b-e
D × E	46.8b-e	19.9b-g	78.3i	29.8e	39.4ab	46.5j	9.3i
D × F	48.1c-e	19.0b-g	74.0g	25.5b-e	39.8a-d	44.3e	9.6j
D × G	47.1b-e	18.5b-f	69.0b-i	26.3b-e	39.4ab	43.6c	7.3c-f
D × H	44.8b-e	18.0a-f	71.0e-i	26.8b-f	40.2b	41.6a-c	6.2bc
E × F	45.5b-e	18.9b-g	66.8a-h	25.0b-e	39.9a-d	43.7d-i	7.7d-h
E × G	46.8b-e	24.4g	77.0h	36.0g	39.2a	42.5a-e	7.8d-h
E × H	44.7b-e	19.7b-g	73.3g	28.5c-g	39.3ab	42.5a-e	7.6d-h
F × G	43.4b-e	18.5b-f	67.5a-h	26.8b-f	39.8a-d	43.9e	7.1c-e
F × H	45.9b-e	20.1c-g	66.3a-g	26.0b-e	39.6a-d	42.9a-f	7.7d-h
G × H	43.4b-e	18.5b-f	70.8e-i	29.3e-g	40.0a-e	43.5b-h	5.8b
平均值	45.8	18.8	67.6	25.3	39.4	43.6	7.5

(Continued)

供試組合	果 重 (g)	果 長 (cm)	果 寬 (cm)	果肉厚 (cm)	株 高 (cm)	節長間長 (cm)	側蔓數
A × B[z]	545.3a[y]	22.7a	6.4a	1.5a	138.4a	9.3i-l	0.6a
A × C	598.5b	23.2ab	6.4a	1.5a	142.0ab	8.3c-f	0.4a
A × D	602.2bc	24.1bc	6.4a	1.5a	149.2bc	8.6d-h	1.1a-c
A × E	609.4bc	25.0c	6.5ab	1.5a	158.6cd	8.8f-j	2.6e-i
A × F	610.3bc	26.4d	6.5ab	1.5a	160.1de	8.1b-e	1.4a-e
A × G	613.8bc	26.4d	6.5ab	1.5a	160.5de	8.9f-k	0.9ab
A × H	630.1b-d	26.5d	6.5ab	1.6ab	160.9de	7.1a	2.5d-h
B × C	642.5b-e	26.7de	6.6a-c	1.6ab	161.6de	9.7l	0.9ab
B × D	649.5c-e	26.8d-f	6.6a-c	1.6ab	161.9de	9.4j-l	0.4a
B × E	668.1d-g	27.3d-g	6.6a-c	1.6ab	166.7d-f	9.2h-l	2.5d-h
B × F	673.0d-h	27.5d-g	6.6a-c	1.6ab	168.7e-g	8.3c-f	2.3c-g
B × G	679.7d-h	27.7e-h	6.6a-c	1.6ab	169.4e-g	9.3i-l	1.5a-f
B × H	681.5e-h	27.7e-h	6.6a-c	1.6ab	171.9f-h	9.7l	1.4a-e
C × D	682.2e-h	27.9f-i	6.6a-c	1.6ab	174.2f-h	9.3i-l	0.8a
C × E	684.8e-i	28.0g-i	6.7b-d	1.6ab	176.7g-i	9.5kl	2.7f-i
C × F	686.4e-i	28.0g-i	6.7b-d	1.6ab	176.9g-i	8.1b-e	1.3a-d
C × G	687.4e-i	28.1g-j	6.7b-d	1.7bc	177.6g-i	8.9f-k	1.3a-d
C × H	690.9e-j	28.7h-k	6.7b-d	1.7bc	178.0g-i	7.9bc	0.6a
D × E	708.4f-k	28.8h-k	6.7b-d	1.7bc	180.2h-j	7.5ab	4.8g
D × F	716.0f-k	28.9i-k	6.7b-d	1.7bc	180.3h-j	8.9f-k	3.8ig
D × G	717.9f-k	29.0i-k	6.8c-e	1.7bc	184.7i-k	8.5c-g	1.2a-c
D × H	719.1g-k	29.2j-l	6.8c-e	1.7bc	185.0i-l	8.9f-k	0.7a
E × F	728.3h-k	29.5kl	6.9de	1.8cd	185.2i-l	8.0b-d	3.1g-i
E × G	734.5i-k	30.2lm	6.9de	1.8cd	185.7i-l	8.4c-g	3.7g-i
E × H	738.7j-k	30.5mn	6.9de	1.8cd	188.5j-l	8.6d-h	2.8g-i
F × G	740.3j-k	31.4no	6.9de	1.9d	189.5j-l	8.0b-d	3.0g-i
F × H	745.3kl	31.8o	7.0e	1.9d	193.0j-l	8.1b-e	1.5a-f
G × H	792.6l	32.1o	7.0e	1.9d	194.4l	8.7e-i	2.1b-g
平均值	677.7	28.2	6.7	1.7	172.2	8.6	1.8

[z] A：Nung Fa 18，B：Chu-Shan Joong，C：Pai-Tsai-Kua jie，D：Tung kua Ching
E：Shuang-Tou-Chyi，F：Taipei Yuh，G：Green Bowl inbred，H：Tai-chung Mu Kua。

[y] Means in columns followed by a common letter do not differ significantly at the 5% level, according to Duncan's multiple-range test.

二、品系比較試驗

12個優良組合進行品系比較試驗，結果由表 3 得知，農試123號、127號、132號、183號、338號、425號、524號和781號等組合之產量和果數均較商業對照品種萬綠（F_1）爲高，綜合評估其他園藝性狀如雌花始花期、果實色澤、果實形狀、品質、苦味和田間感病情形等，均以農試132號和農試183號爲最佳之雜交組合。

表 3. 品系比較試驗特性及產量調查表（77年春作）

Table 3. Comparision of yield and horticultural characters of lines in spring crop 1988[y]

品種或品系	生長勢	產量（Kg/0.1ha）		果數（條/0.1ha）		lst ♂	lst ♀	lst ♀	果 重
		採收頭 7 天	總產量	採收頭 7 天	總果數	開花天數	開花天數	著生節位	(g)
農試123號	強	1,380ab[z]	2,470b-e	1,950a-d	3,480b-d	30.7ab	29.5ab	4.6a-c	785.9b-d
農試124號	中	1,140a	2,050a-c	1,350a	2,930ab	33.6c	37.9e	9.3e	848.6de
農試127號	強	1,530abc	2,960e-f	2,000b-d	3,980d-f	30.1ab	30.6a-c	4.5ab	816.8c-e
農試128號	中	1,150a	1,940a	1,580ab	2,780a	31.0a-c	35.6de	6.8d	684.5a
農試129號	強	1,470abc	2,240a-c	2,030b-d	3,100a-c	29.4a	32.1b-d	5.5a-d	768.2bc
農試130號	中	1,200a	2,220a-c	1,650a-c	3,350a-d	31.1a-c	34.2c-e	6.3cd	799.4b-d
農試132號	強	1,790bc	3,090f	2,550d	4,430f	32.0bc	30.6a-c	4.5ab	770.5bc
農試183號	強	1,650bc	2,930d-f	2,430bc	4,400d	28.9a	27.9a	4.2a	731.1ab
農試338號	強	1,520abc	2,620c-f	1,980b-d	3,500b-d	31.5a-c	32.6b-d	5.3a-d	814.0cd
農試425號	強	1,500abc	2,510b-f	2,000b-d	3,480b-d	32.4bc	35.3de	5.7a-d	800.1b-d
農試524號	強	1,880c	2,860d-f	2,200b-d	3,650cd	30.6ab	29.3ab	5.4a-d	854.0de
農試781號	強	1,500abc	2,590c-f	2,120b-d	3,750c-e	30.8ab	31.4a-c	4.6a-c	767.2bc
萬綠(CK)	強	1,410ab	2,420a-d	2,280d	3,330a-c	29.3a	33.0b-d	5.9a-d	752.3a-d

(Continued)

品種或品系	果 長 (cm)	果 寬 (cm)	果肉厚 (cm)	果心長 (cm)	果心寬 (cm)	株 高 (cm)	節間長 (cm)	側蔓數 (cm)	田間病害發生情形		
									病毒病	露菌病	白粉病
農試123號	28.4b	6.3bc	1.9bc	23.2b	3.1b-d	237.4a-c	9.4ab	0.7ab	輕微	輕微	輕微
農試124號	31.7ef	6.1b	1.9c	27.7f	2.8a	249.6b-d	10.0bc	0.5a	中等	中等	輕微
農試127號	31.7ef	6.1b	1.8ab	26.0de	3.1b-d	249.0b-d	10.0bc	1.4b-e	輕微	輕微	輕微
農試128號	29.2bc	6.2bc	1.7a	24.9cd	3.2cd	286.0e	11.4d	1.6c-e	中等	中等	輕微
農試129號	32.1f	5.8a	1.8ab	26.5e	3.0a-c	231.5ab	9.3ab	0.9a-d	輕微	輕微	中等
農試130號	30.3c-e	6.2bc	1.8ab	25.9de	3.0a-c	249.5b-d	10.0bc	0.8a-c	中等	輕微	輕微
農試132號	26.4a	6.6b	1.9bc	21.7a	3.1f	233.8a-c	9.4ab	1.6c-e	輕微	輕微	輕微
農試183號	30.9bc	6.1b	1.8ab	23.1b	3.3d	235.6a-c	9.4ab	0.9a-d	輕微	輕微	輕微
農試338號	31.5d-f	6.1b	1.8ab	26.1e	2.9ab	256.7cd	10.3b-d	0.9a-d	輕微	輕微	輕微
農試425號	28.1b	6.4cd	1.7a	23.6b	3.2cd	245.5a-c	9.8ab	1.7de	輕微	輕微	輕微
農試524號	30.2c-e	6.4cd	2.0c	24.0bc	2.8a	243.4a-c	9.7ab	1.0a-d	輕微	輕微	輕微
農試781號	29.2bc	6.2bc	1.8ab	23.6b	3.3d	217.6a	8.7a	0.3ac	輕微	輕微	輕微
萬綠(CK)	28.4b	6.2bc	1.8a	23.3b	2.9ab	221.1ab	8.8a	1.5b-e	中等	中等	輕微

[z] Means in columns followed by a common letter do not differ significantly at the 5% level, according to Duncan's multiple-range test.

[y] Sowing date：March 20.1988.

三、品系區域試驗

㈠春作

1. 78年春作：本項試驗結果詳如表 4。在霧峰鄉所進行的試驗，無論在產量和果數，農試183號與對照品種差異不顯著，然而在崙背鄉卻以農試183號的產量最高且差異顯著。其他園藝性狀如果重、果長、果肉硬度，果皮硬度等均較栽培品種為優且差異顯著，田間自然發病情形亦以農試183號較為輕微。
2. 80年春作：本項試驗結果如表 5。農試183號在二處之平均早產量和總產量分別為1,024.6公斤／公畝和3,261.4公斤／公畝，較對照品種萬綠之688公斤／公畝2,899.8公斤／公畝，分別高出48.8%和12.5%。
3. 81年春作：本項試驗結果如表 6。農試183號在霧峰鄉和大埤鄉二處之採收期頭 7 天產量均較對照品種為高，且差異顯著，總產量卻與對照品種大致相同，差異不顯著。在鹽埔鄉雖然頭 7 天產量與對照品種相似，但總產量卻比對照品種高，且達差異顯著。

表 4. 農試183號區域試驗之特性及產量調查（78年春作）

Table 4. Yield and horticultural characters of Nung-shi 183 in regional trials in spring crop 1989[y]

地區	品種或品系	產量 (Kg/0.1ha)		果數 (條/0.1ha)		糖度	果重
		採收頭7天	總產量	採收頭7天	總果數	(Brix)	(g)
農試所	農試132號	1,094.0a[z]	3,809.5b	1,156.8a	4,369.0c	3.90c	947.3ab
	農試183號	1,115.5a	3,466.3ab	1,175.0a	3,900.0ab	3.83abc	1,018.4b
	綠豐 (CK1)	1,024.8a	3,504.0ab	1,080.8a	3,987.8abc	3.68a	906.4a
	萬綠 (CK2)	1,075.0a	3,203.3a	1,138.0a	3,718.5a	3.70ab	907.5a
崙背鄉	農試132號	1,152.5b	4,646.3b	2,360.0b	5,975.8b	3.90a	873.8ab
	農試183號	1,545.8c	5,716.5c	2,923.8c	6,951.5c	3.90a	910.7b
	綠豐 (CK1)	731.8a	3,323.3a	1,621.8a	4,378.0a	3.75a	852.9ab
	萬綠 (CK2)	996.8ab	4,192.3b	2,125.0ab	5,420.8b	3.80a	805.7a

(Continued)

地區	品種或品系	果長 (cm)	果寬 (cm)	果心長 (cm)	果肉厚 (cm)	果肉硬度 (8mm)	果皮硬度 (8mm)	田間病害發生情形		
								病毒病	露菌病	白粉病
農試所	農試132號	27.00a	7.68c	3.47b	2.10ab	4.97c	80.50a	輕微	輕微	輕微
	農試183號	32.58c	7.28a	3.38ab	1.97a	5.28d	83.00b	輕微	輕微	輕微
	綠豐(CK1)	27.65ab	7.38ab	3.38ab	2.02ab	4.43a	79.50a	中等	中等	輕微
	萬綠(CK2)	28.22b	7.43b	3.17a	2.15b	4.70b	80.75ab	輕微	中等	輕微
崙背鄉	農試132號	27.75a	7.23b	3.47b	1.97a	4.82b	80.00ab	輕微	輕微	輕微
	農試183號	32.20b	7.00ab	3.43b	1.98a	5.05b	82.25c	輕微	輕微	輕微
	綠豐(CK1)	29.05a	7.03ab	3.38ab	1.88a	4.32a	78.75a	中等	中等	輕微
	萬綠(CK2)	28.88a	6.88a	3.18a	1.97a	4.40a	81.25b	輕微	輕微	輕微

[z] Means in columns followed by a common letter do not differ significantly at the 5% level, according to Duncan's multiple-range test.
[y] Sowing date：March 17.1989.

表 5. 農試183號區域試驗之產量及果數分析 (80年春作)

Table 5. Performances of Nung-shi 183 in regional trials in spring crop 1991[y]

地區	品種(系)	產量 (Kg/0.1ha)		果數 (條/0.1ha)	
		採收頭7天	總產量	採收頭7天	總果數
農試所	農試132號	790.50b[z]	2,726.00a	1,069.25b	3,937.25a
	農試183號	813.25b	2,978.75b	1,091.00b	4,353.50b
	綠豐 (CK1)	678.00a	3,061.75b	952.25a	4,507.00b
	萬綠 (CK2)	692.00a	3,042.75b	963.25a	4,519.00b
大埤鄉	農試132號	973.50b	3,205.25ab	1,617.50b	5,354.00a
	農試183號	1,236.00c	3,544.00b	1,928.00c	5,581.25a
	綠豐 (CK1)	604.25a	2,770.75a	998.50a	4,806.75a
	萬綠 (CK2)	684.00a	2,756.75a	1,057.50a	4,863.25a

[z] Means in columns followed by a common letter do not differ significantly at the 5% level, according to Duncan's multiple-range test.

[y] TARI sowing date : March 20.1991. harvesting date : May 04-June 02.1991.
Tapi sowing date : March 24.1991. harvesting date : May 05-June 09.1991.

表 6. 農試183號區域試驗之產量及果數調查分析 (81年春作)

Table 6. Performances of Nung-shi 183 in regional trials in spring crop 1992[y]

地區	品種(系)	產量 (Kg/0.1ha)		果數 (條/0.1ha)	
		採收頭7天	總產量	採收頭7天	總果數
霧峰鄉	農試132號	611.00b[z]	2,527.50a	751.25a	3,633.50a
	農試183號	707.00c	3,052.00b	885.00a	4,375.75b
	綠豐 (CK1)	482.25a	2,895.35ab	600.00a	4,160.00b
	萬綠 (CK2)	643.50b	3,004.00b	870.50a	4,178.25b
大埤鄉	農試132號	1,377.50b	4,774.50a	1,830.00b	6,415.00a
	農試183號	1,307.75b	4,869.50a	1,730.00ab	6,520.00a
	綠豐 (CK1)	1,150.50a	5,299.50a	1,530.00a	6,745.00a
	萬綠 (CK2)	1,189.00a	4,798.50a	1,620.00ab	6,480.00a
鹽埔鄉	農試132號	1,040.00b	3,750.00a	1,440.00b	5,360.00a
	農試183號	1,177.00b	4,852.00b	1,500.00b	6,430.00b
	綠豐 (CK1)	631.00a	4,004.00a	840.00a	5,780.00ab
	萬綠 (CK2)	1,000.00b	3,896.00a	1,260.00b	5,380.00a

[z] Means in columns followed by a common letter do not differ significantly at the 5% level, according to Duncan's multiple-range test.

[y] Wufeng sowing date : March 25. 1992. harvesting date : May 11-June 10. 1992.
Tapi sowing date : March 10. 1992. harvesting date : April 22-May 24. 1992.
Yenpu sowing date : March 20. 1992. harvesting date : May 01-31. 1992.

4. 82年春作：本項試驗結果，詳如表 7。農試183號在霧峰鄉、大埤鄉和鹽埔鄉等地之平均採收頭 7 天產量和總產量分別爲1,177.25公斤／公畝和4,072.67公斤／公畝，較對照品種萬綠之1,066.42公斤／公畝和3,903.83公斤／公畝爲高，其中以鹽埔鄉之總產量4,479公斤／公畝最高。

表 7. 農試183號區域試驗之產量及果數調查結果（82年春作）

Table 7. Performances of Nung-shi 183 in regional trials in spring crop 1993[y]

地區	品種(系)	產量 (Kg/0.1ha)		果數 (條/0.1ha)	
		採收頭7天	總產量	採收頭7天	總果數
霧峰鄉	農試132號	1,510.00a[z]	3,447.50a	2,190.00a	5,260.00a
	農試183號	1,660.00b	3,805.50b	2,240.00a	5,910.00b
	綠豐 (CK1)	1,523.50a	3,642.25ab	2,110.00a	5,530.00ab
	萬綠 (CK2)	1,518.50a	3,391.50a	2,220.00a	5,330.00a
大埤鄉	農試132號	787.50b	4,083.75b	908.00a	4,838.00ab
	農試183號	815.00b	3,933.50a	932.00a	4,795.50ab
	綠豐 (CK1)	745.25a	3,712.25a	911.50a	4,612.50a
	萬綠 (CK2)	818.00b	4,284.50b	942.00a	4,868.25b
鹽埔鄉	農試132號	1,023.00a	4,183.00a	1,160.00a	5,320.00ab
	農試183號	1,056.75b	4,479.00b	1,090.00a	6,200.00c
	綠豐 (CK1)	807.00a	4,372.00b	900.00a	5,890.00bc
	萬綠 (CK2)	862.75a	4,036.00a	909.00a	5,280.00a

[z] Means in columns followed by a common letter do not differ significantly at the 5% level, according to Duncan's multiple-range test.

[y] Wufeng sowing date : March 03. 1993. harvesting date : April 29-May 30. 1993.
Tapi sowing date : Feb. 25. 1993. harvesting date : March 31-April 29. 1993.
Yenpu sowing date : Feb. 16. 1993. harvesting date : April 03-May 02. 1993.

(二)秋作

1. 78年秋作：試驗結果詳如表 8。在霧峰鄉農試183號之產量和果數與對照品種差異不顯著；在崙背鄉農試183號之產量較高，比對照品種萬綠高出30%，其他園藝性狀和田間自然發病等均與栽培品種略同。

表 8. 農試183號區域試驗之特性及產量調查結果（78年秋作）

Table 8. Yield and horticultural characters of Nung-shi 183 in regional trials in fall crop 1989[y]

地區	品種或品系	產量 (Kg/0.1ha)		果數 (條/0.1ha)		糖度	果重
		採收頭7天	總產量	採收頭7天	總果數	(Brix)	(g)
農試所	農試132號	746.0b[z]	1,801.8a	1,162.5b	3,050.0a	3.92a	746.2a
	農試183號	848.0b	1,924.0ab	1,237.5b	3,000.0a	3.85a	792.1a
	綠豐 (CK1)	276.5a	2,076.0ab	387.5a	3,275.0a	3.70a	759.0a
	萬綠 (CK2)	764.0b	2,176.0b	1,100.0b	3,512.5a	3.73a	746.5a
崙背鄉	農試132號	237.5a	2,360.0ab	388.5a	3,767.5ab	3.92b	819.8a
	農試183號	359.3c	3,017.0c	570.5b	4,562.3b	3.78ab	899.8b
	綠豐 (CK1)	347.0bc	2,962.0bc	534.3b	4,557.5b	3.63a	812.5a
	萬綠 (CK2)	303.8b	2,313.0a	487.8b	3,570.0a	3.63a	848.4ab

(Continued)

地區	品種或品系	果長 (cm)	果寬 (cm)	果心長 (cm)	果肉厚 (cm)	果肉硬度 (8mm)	果皮硬度 (8mm)	田間病害發生情形		
								病毒病	露菌病	白粉病
農試所	農試132號	27.93a	6.68a	3.50c	1.90a	4.75b	80.50ab	輕微	輕微	輕微
	農試183號	31.88c	6.68a	3.40bc	1.90a	4.82b	82.00b	輕微	輕微	輕微
	綠豐(CK1)	29.78b	6.68a	3.35b	1.90a	4.23a	79.00a	中等	中等	輕微
	萬綠(CK2)	29.60b	6.50a	3.15a	1.88a	4.28a	80.50ab	輕微	中等	輕微
崙背鄉	農試132號	27.17a	7.13a	3.50b	2.02a	4.90c	81.00a	輕微	輕微	輕微
	農試183號	32.25c	6.95a	3.35b	1.90a	5.05c	82.75b	輕微	輕微	輕微
	綠豐(CK1)	28.38ab	7.03a	3.35b	2.05a	4.33a	79.75a	中等	中等	輕微
	萬綠(CK2)	28.95b	7.05a	3.15a	2.05a	4.57b	80.00a	輕微	輕微	輕微

[z] Means in columns followed by a common letter do not differ significantly at the 5% level, according to Duncan's multiple-range test.
[y] Sowing date : Oct. 05. 1989.

2. 79年秋作：試驗結果詳如表 9。在農試183號在霧峰鄉和九如鄉等地之平均採收頭 7 天產量和總產量分別為1,415.25公斤／公畝和3,540.38公斤／公畝，較對照品種萬綠之1,023.75公斤／公畝和2,929.25公斤／公畝分別高出38%和21%。

表 9. 農試183號區域試驗之產量及果數調查結果 (79年秋作)

Table 9. Performances of Nung-shi 183 in regional trials in fall crop 1990[y]

地區	品種(系)	產量 (Kg/0.1ha)		果數 (條/0.1ha)	
		採收頭 7 天	總產量	採收頭 7 天	總果數
霧峰鄉	農試132號	1,262.50ab[z]	2,376.00a	1,616.25ab	3,386.75b
	農試183號	1,472.00b	2,185.00a	1,842.50b	3,063.25a
	綠豐 (CK1)	1,383.75ab	2,325.25a	1,686.75ab	3,213.75ab
	萬綠 (CK2)	1,060.00a	2,134.50a	1,306.00a	3,111.50a
九如鄉	農試132號	1,337.25b	4,051.50b	2,166.75b	6,291.75b
	農試183號	1,358.50b	4,894.75c	2,008.25b	6,925.00c
	綠豐 (CK1)	803.00a	4,039.25b	1,108.25a	6,125.25b
	萬綠 (CK2)	987.50a	3,724.00a	1,425.00a	5,675.00a

[z] Means in columns followed by a common letter do not differ significantly at the 5% level, according to Duncan's multiple—range test.
[y] TARI sowing date : Sept. 09. 1980. harvesting date : Nov. 05～Dec. 03. 1980.
Chiuju sowing date : Oct. 16. 1980. harvesting date : Nov. 28～Dec. 30. 1980.

3. 81年秋作：分別在霧峰鄉、大埤鄉及鹽埔鄉等地區進行區域試作，結果如表10。農試183號在 3 個試區之產量均較對照品種萬綠為高，3 個試區之平均產量較對照品種高出14%。

表 10. 農試183號區域試驗之產量及果數調查結果（81年秋作）

Table 10. Performances of Nung-shi 183 in regional trials in fall crop 1992[y]

地區	品種(系)	產量 (Kg/0.1ha)		果數 (條/0.1ha)	
		採收頭7天	總產量	採收頭7天	總果數
霧峰鄉	農試132號	1,291.50a[z]	3,174.25a	1,680.00ab	4,320.00a
	農試183號	1,592.00b	3,946.00a	1,960.00b	5,120.00a
	綠豐 (CK1)	1,364.00a	3,573.25a	1,660.00a	4,660.00a
	萬綠 (CK2)	1,488.50a	3,317.00a	1,810.00ab	4,220.00a
大埤鄉	農試132號	993.25ab	4,988.75a	1,326.25b	6,521.50a
	農試183號	1,037.50b	5,514.25b	1,312.75b	6,721.75a
	綠豐 (CK1)	839.25a	5,225.00ab	1,069.50a	6,511.75a
	萬綠 (CK2)	903.50ab	5,079.00ab	1,179.50ab	6,481.75a
鹽埔鄉	農試132號	438.75b	4,187.75a	674.75b	5,891.25b
	農試183號	444.75b	5,144.50b	600.75a	5,631.75ab
	綠豐 (CK1)	387.75a	4,486.50a	552.75a	5,369.00a
	萬綠 (CK2)	396.50a	4,378.00a	604.25a	5,647.00ab

[z] Means in columns followed by a common letter do not differ significantly at the 5% level, according to Duncan's multiple-range test.

[y] Wufeng sowing date : Oct. 06. 1992. harvesting date : Nov. 19～Dec. 18. 1992.
Tapi sowing date : Aug. 10. 1992. harvesting date : Sept. 22～Oct. 24. 1992.
Yenpu sowing date : Aug. 14. 1992. harvesting date : Sept. 28～Nov. 01. 1992.

四、產量和果數穩定性分析

將81年及82年區域試驗3個地點4個品種（系）之產量和果數，進行穩定性分析，農試183號以每公畝產量和果數分別為4,131.9公斤和5,688.5條居於最高（表11）。農試132號、農試183號、綠豐及萬綠之產量直線迴歸係數，分別為1.070、0.933、1.130及0.866，顯示四品種（系）均具有良好的穩定性(圖 1)；農試132號、農試183號、綠豐及萬綠之果數直線迴歸係數，分別為1.034、1.024、1.086及0.856，顯示除萬綠為果數較少而不穩定外，其餘三個品種(系)均具有良好的穩定性(圖 2)

表 11. 胡瓜農試183號在霧峰鄉、大埤鄉和鹽埔鄉等試區之產量和果數之穩定性

Table 11. Yield and fruits stability of Nung-shi 183 in regional trials at 3 locations during spring crop 1992 and 1993.

品種(系)	產量 (Kg/0.1ha)	產量在試區3地點之迴歸係數	果數 (Kg/0.1ha)	產量在試區3地點之迴歸係數
農試132號	3,794.4a[z]	1.070	5,137.8a	1.034
農試183號	4,131.9c	0.933	5,688.5 d	1.024
綠豐 (CK1)	3,987.5b	1.130	5,452.2c	1.086
萬綠 (CK2)	3,901.8b	0.866	5,252.8b	0.856

[z] Means in columns followed by a common letter do not differ significantly at the 5% level, according to Duncan's multiple-range test.

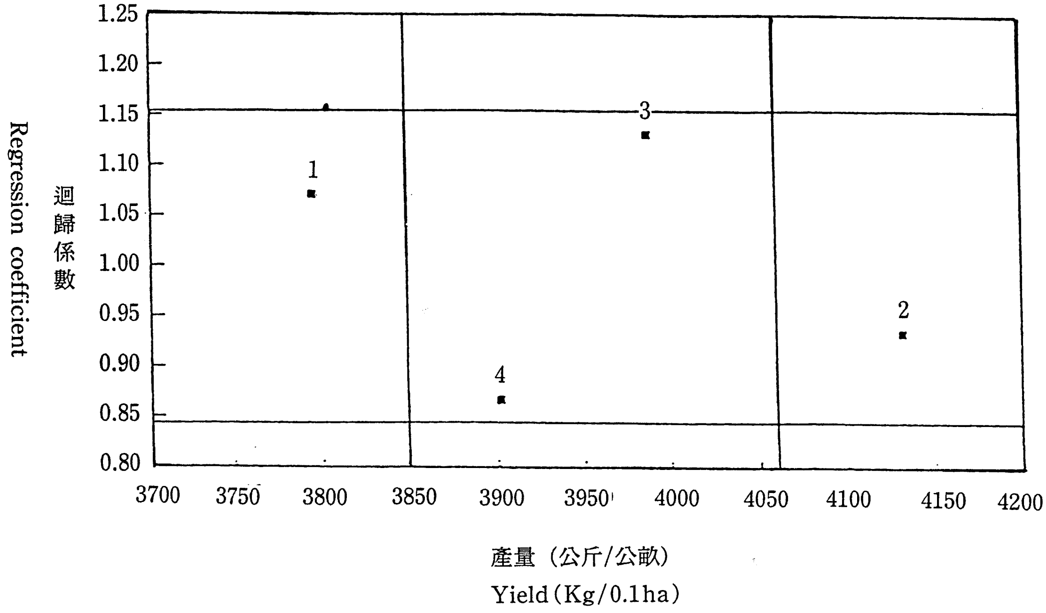

圖 1. 農試183號在 3 個區域地點之產量及穩定性關係
Fig. 1. The relation of yield performance and stability of 4 cucumber hybrids grown at 3 locations during spring crop 1992 and 1993

No. 1 : Nung-shi 132, No. 2 : Nung-shi 183. No.3 : Lufeng, No. 4 : Green Bowl

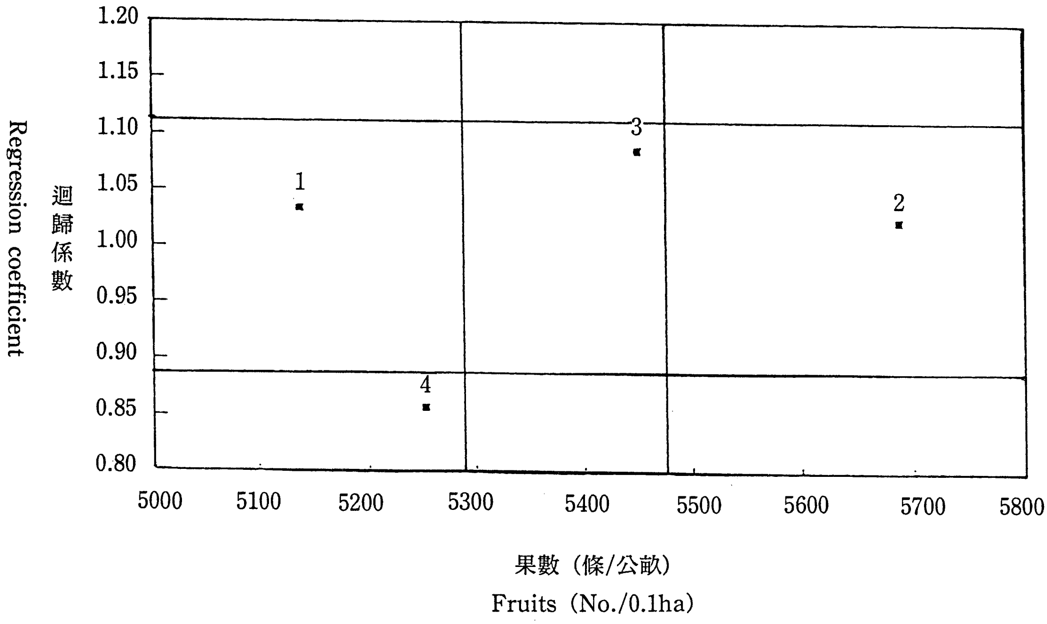

圖 2. 農試183號在 3 個區域地點之果數及穩定性關係
Fig. 2. The relation of fruits performance and stability of 4 cucumber hybrids grown at 3 locations during spring crop 1992 and 1993

No. 1 : Nung-shi 132, No. 2 : Nung-shi 183. No.3 : Lufeng, No. 4 : Green Bowl

五、抗病性檢定

(一)白粉病抗病性檢定

在溫室內模擬天然條件下接種，病原孢子經由風力四處散佈，自然感染農試183號以及其親本和對照品種幼苗上，接種後二週、三週和四週各調查一次，以三次調查的發病指數之平均值作爲抗病性評估之依據，根據檢定結果農試183號對白粉病之發病指數爲26.7，抗病性屬中抗（表12）。

(二)露菌病抗病性檢定

農試183號等品種在幼苗期 5 片本葉時，利用人工接種方式，將露菌病孢子懸浮液噴灑到幼苗上，一週後調查植株由頂部向下之 5 個葉片之發病情形，根據檢定結果農試183號對露菌病之發病指數爲29.3，抗病性屬中抗（表12）。

(三)病毒病抗病性檢定

農試183號以及對照品種等，經胡瓜嵌紋病毒、木瓜輪點病毒一西瓜系統及矮南瓜黃化嵌紋病毒等病毒分別單獨接種後，其抗病性檢定結果詳如表12。農試183號對胡瓜嵌紋病毒和木瓜輪點病毒一西瓜系統具有抗性，發病指數分別爲13.7和18.0，對矮南瓜黃化嵌紋病毒爲中抗，發病指數爲28.7。

表 12. 農試183號人工接種抗病性檢定結果

Table 12. Disease resistance of Nung-shi 183 tested by artificial inoculation[z].

病害 / 品種(系)	白粉病	露菌病	胡瓜嵌紋病毒	木瓜輪點病毒一西瓜系統	矮南瓜黃化嵌紋病毒
農試183號	中抗 (26.7)[y]	中抗 (29.3)	抗 (13.7)	抗 (18.0)	中抗 (28.7)
綠豐 (CK1)	感 (40.8)	感 (45.2)	中抗 (27.0)	感 (42.0)	極感 (61.7)
萬綠 (CK2)	中感 (33.3)	中感 (35.0)	抗 (10.7)	中抗 (22.0)	中感 (37.6)

[z] Screening for resistance to powdery mildew : sowing date : March 09. 1993. inoculating date : March 16. 1993.

Screening for resistance to downy mildew : sowing date : April 19. 1993. inoculating date : May 01. 1993.

Screening for resistance to viruses : sowing date : March 03. 1991. inoculating date : March 12. 1991.

[y] Values in the parenthesis are indexs of disease incidence.

六、果實測定

(一)果實顏色變化之測定

胡瓜果實採收後貯放在室溫下，顏色的轉變快慢，會影響到商品售價，一般果色轉變成淡綠色時，售價較差。由色差計的讀值，得知農試183號採收後放置在室溫一星期後，顏色的轉變不大，由圖3，L 值亮度變化情形來看，農試183號經過七天後，其亮度仍有34%。a 值呈負值時，表示綠色，b 值呈正值時，表示藍色，a 值的減少和 b 值的增加，表示濃綠色增加，圖 4 和圖 5 分別爲 a 值和 b 值的變化，一週後，a 值由−5.37減少爲−9.39，而 b 值由5.97增加爲11.15，綜合顯示 L 值、a 值和 b 值 等數字的分析結果，得知農試183號雖經一週之貯放，果皮顏色仍然維持相當的濃綠。

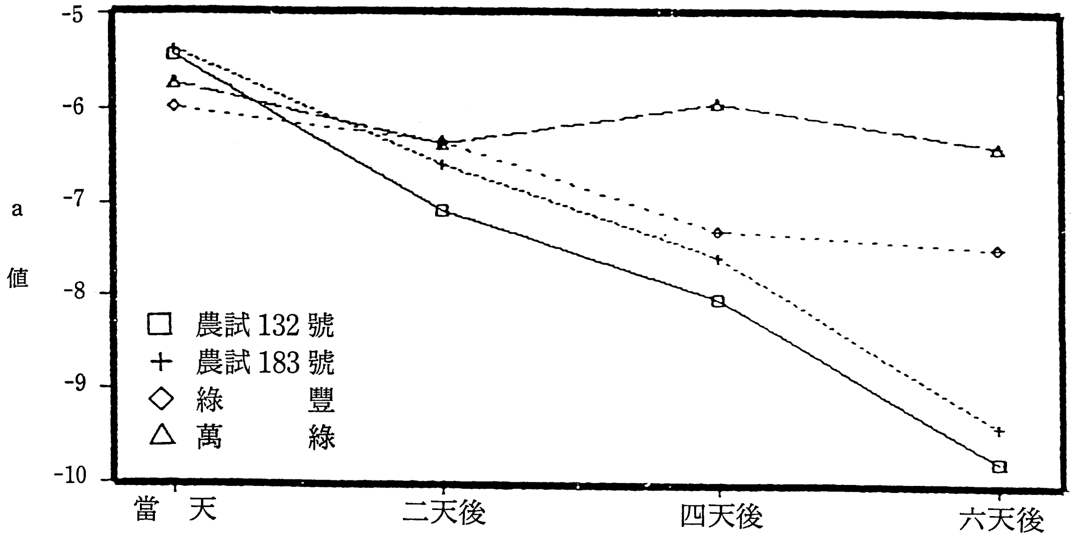

圖 3. 農試183號果實採收貯放在室溫下之 a 值變化
Fig. 3. Effect on the a value (redness) of Nung-shi 183's fruits storage at room temperature

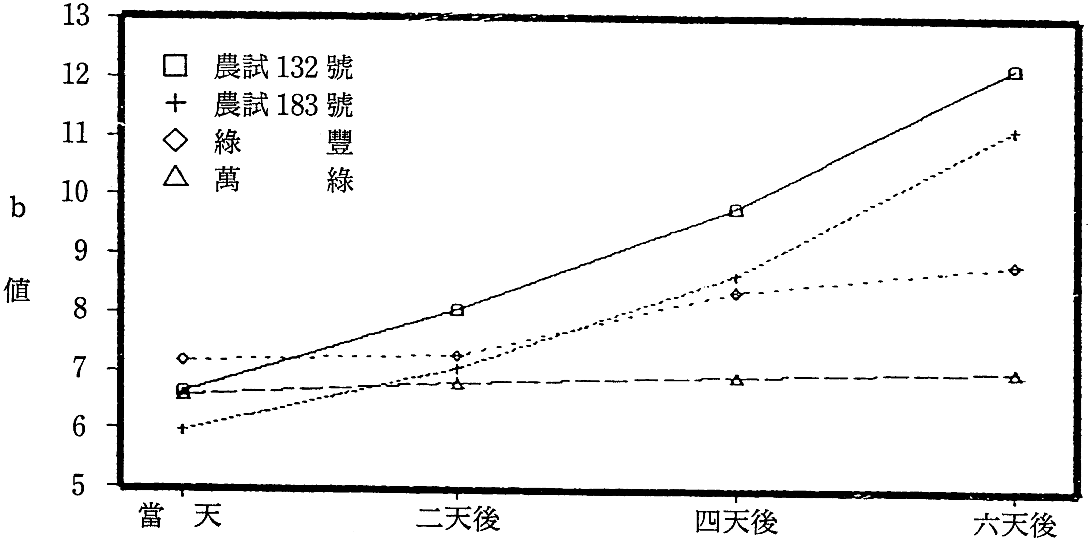

圖 4. 農試183號果實採收貯放在室溫下之 b 值變化
Fig. 4. Effect on the b value (yellowness) of Nung-shi 183's fruits storage at room temperature

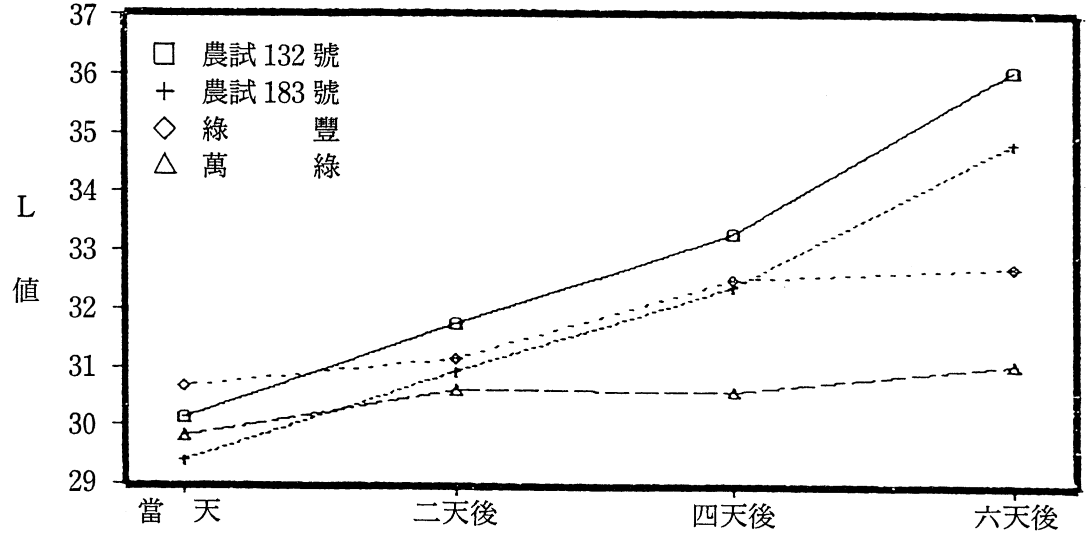

圖 5. 農試183號果實採收後貯放在室溫下之 L 值變化
Fig. 5. Effect on the L value (brightness) of Nung-shi 183's fruits storage at room temperature

(二)果實失重率之測定

胡瓜果實含水量高達90%[9]，一般胡瓜果實採收後放置在室溫下數日，果實表面會因失水而發生縐縮現象，影響商品價值。由圖 6 得知，農試183號在室溫下貯放一週，其相對失水量較對照品種爲少，果皮沒有縐縮，仍具有商品價值。

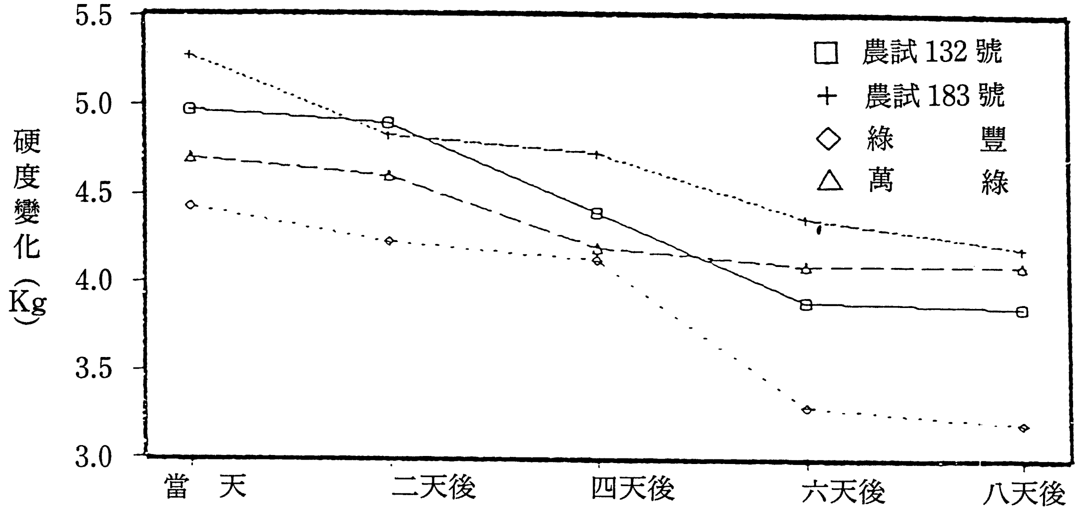

圖 6. 農試183號果實採收後貯放在室溫下之損失重百分率
Fig. 6. Effect of weight loss of Nung-shi 183's fruits storage at room temperature

㈢果實硬度變化之測定

胡瓜採收後果實失水率的快慢和肉質硬度的變化，會影響果實品質和貯存壽命，一般而言，失水較慢和果肉較硬的果實，其貯放壽命較長[8]。由圖 7 得知，農試183號在室溫下存放一週，果實硬度雖有下降，但與採收當日的硬度差異不大。

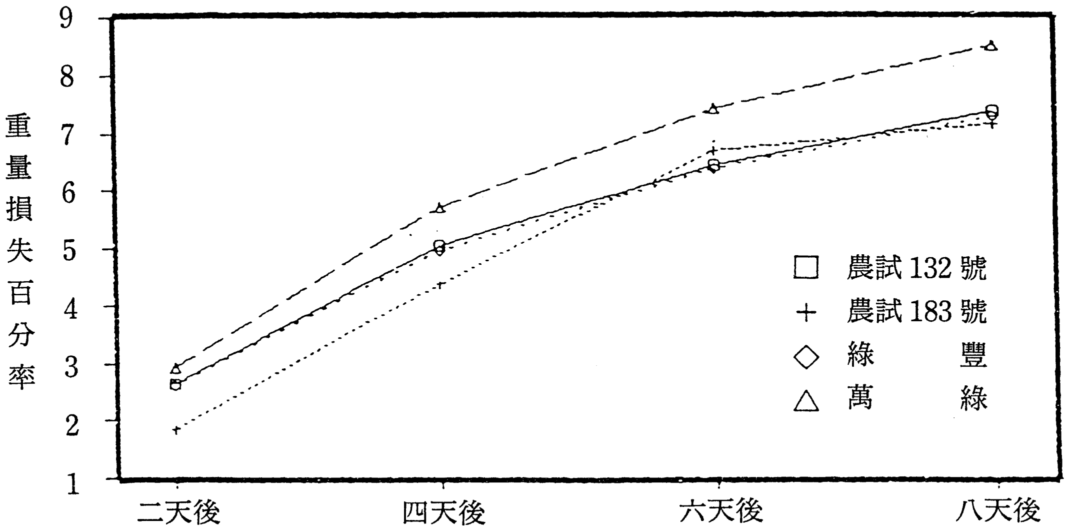

圖 7. 農試183號果實採收後貯放在室溫下之硬度變化
Fig. 7. Effect on hardeness of Nung-shi 183's fruits storage at room temperature

綜合上述各項測試結果，農試183號爲果色濃綠、果肉較硬、耐貯存的品種。

七、品種特性

農試183號（臺農一號）爲黑皮大胡瓜一代雜交品種，果形美觀，果長32.4公分，果寬6.9公分，較一般栽培品種爲長，果重約700公克左右，果實品質良好，果實無苦味，果色濃綠，果刺白色細少，果皮無網紋和條溝，果心較小，果肉較硬，在室溫下貯放一星期，果實色澤依然明亮和濃綠，仍具商品價值，果實相對失水率亦低，爲一耐貯運胡瓜品種。雌花開花時期較早，從播種至開第一朶雌花春、夏作僅需32天，秋作34天，第一朶雌花著生在 4 ～ 5 節。田間直播至採收，春作和夏作爲44～45天，秋作爲47～49天，開花至採收，春作和夏作爲12～13天，秋作爲13～15天。採收頭七天之早產量約佔總產量的2／5～3／5，較一般栽培品種高出12.8%。產量穩定性亦佳，每分地產量約4,000公斤左右。臺農一號具有抗胡瓜嵌紋病毒和木瓜輪點病毒—西瓜系統、中抗矮南瓜黃化嵌紋病毒、露菌病和白粉病等病害。

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Development of Cucumber F_1 Hybrid Tainung No. 1[1]

Wei-Zheng Yang and Chi-Hsiung Hsiao[2]

Summary

Tainung No. 1 is a cucumber F_1 hybrid with Tai-Pei-Yen and Tung-Kua-Ching as its parents those both have been inbred for eight generations. It performs high yield steadily with an average of 4,000 kg/0.1 ha. It has significantly higher yield than the commercial check variety has. The characteristics of Tainung No. 1 are as follows : The first female flower sets at the 4th or 5th node, the days from planting to harvest proximately are 44～45 days in spring and summer and 47～49 days in fall. Fruits are uniform in size, with fine and white spined and dark green skin without net or strips. The flesh is thick with a small seed cavity. It also has good quality and free of bitterness with good storability. Tainung No. 1 is highly resistant to cucumber mosaic virus and type W of papaya ringspot virus. It is also moderately resistant to zucchini yellow mosaic virus, powdery and downy midlew.

Key words : *Cucumis sativus,* Breeding, Tainung No. 1, F_1 hybrid.

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以逢機增殖多型性 DNA 分子標誌鑑別番椒屬野生馴化種原[1]

王昭月[2]　范明仁[2]　羅舜芳[2]　劉新裕[3]

摘要：本試驗以源自日本、美國、巴西和匈牙利等地區之番椒屬14個品系，探討利用逢機增殖多型性 DNA (RAPD) 建立種間之分子標誌，以鑑別番椒屬重要野生馴化種之種原。試驗結果顯示，以 UBC327, UBC346, UBC441及 UBC457等四個隨意引子，經聚合酵素連鎖反應 (PCR)，其 RAPD 之產物具有明顯的多型性表現，且在增殖之多型性 DNA 片段中，可獲得11個有效之多型性 DNA 片段，提供作爲不同「種」辨識之標誌。其中 UBC 327, UBC 346及UBC 457三個引子產生的多型性 DNA 片段，更具有指紋比對之功效，可以清楚地將14個不同品系加以區別。利用上述四個引子產生之所有多型性 DNA 片段，一併進行相似性群集分析 (UPGMA cluster analysis) 之結果顯示，供試的14個品系可分成四個群，第一群包含 2 個品系，屬於 *C. chinense*；第二群包含 4 個品系，屬於 *C. annuum*；第三群包含 5 個品系，也屬於 *C. annuum*；第四群則包含 3 個品系，屬於*C. baccatum*。試驗結果證實，RAPD 標誌對番椒屬具有指紋比對之效，可作爲一種有效且值得信賴之種原鑑別工具。

關鍵詞：逢機增殖多型性 DNA、群集分析、DNA 指紋比對、番椒。

植物遺傳資源保育及有效利用，關係著未來農業生產改進，而種原保育與利用的關鍵，除了識別特殊遺傳特性或評估種原歧異度外，如何開發快速且正確的遺傳特性標誌技術，也是亟須配合發展的要件之一[6]自1984年 Kary Mullis 提出聚合酵素連鎖反應技術 (polymerase chain reaction, PCR)，近十年來已非常廣泛的應用於分子生物研究上，如：(1)探針製備 (probe preparation)，(2)選殖系篩檢 (clone screening)，(3)基因圖譜比對 (mapping)，(4)製備定序用模板 (sequencing template)。唯此利用範圍多針對某特定基因之研究[3]。1990年Williams[15]及 Welsh 等人 (1991)[13]則相繼開始以隨意引子 (arbitrary primer) 進行聚合酵素連鎖反應，使用的引子亦稱爲逢機引子 (random primer)，其多爲10～20個核甘酸序列，之後特將此反應稱爲隨意引子聚合酵素連鎖反應 (arbitrary primer polymerase chain reaction, AP-PCR)，而經此擴增的多型性 DNA 片段則稱爲逢機增殖多型性 DNA 標誌 (random amplified polymorphic DNA marker, RAPD marker)。RAPD 分析方法可應用於遺傳分析標誌、種質鑑定[6,14,16]，或 DNA 指紋比對[11,13]，是一種簡單便利的基因研究工具。

番椒 (pepper, paprika) 是茄科 (Solanaceae) 番椒屬 (*Capsicum*) 一或多年生蔬菜，原產於中、南美洲，如墨西哥、秘魯及瓜地馬拉一帶，據 FAO 1993年調查，全世界有1,224,000公頃的栽

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培面積，其中亞洲地區就占56.5%，因此也是亞洲重要經濟蔬菜之一。番椒果實依辣味有無可分爲二類：有辣味類（pungent），俗稱爲辣椒（hot pepper, chile pepper, chili pepper）；無辣味類（nonopungent）俗稱甜椒（bell pepper, sweet pepper）。

番椒屬內花色、果型分歧很大，故早期「種」的分類很紊亂。曾以花色分成二大群：紫花、白花群；也有依果型特徵分類的[10]，但多屬於較粗放之形態分類，無法正確地臆測「種」間的演化及血緣關係。至目前較廣爲接受的番椒分類，可歸納爲20～30個野生種及 5 個馴化栽培種，此係 Mc Lood 等人（1983）依據植物形態及酵素電泳分析（isozyme electrophoresis）參考歸納的結果[7]，其中五個馴化栽培種爲：*C. annuum*（包含全部甜椒品種及大部分辣椒商業品種）；*C. chinense* Jacqin（辣椒），*C. frutescens* L.，*C. baccatum* L.，及 *C. pubeseens* Ruiz & Pavon。此五個馴化種皆爲人類重要經濟栽培種，前三種更幾乎囊括了全球性主要的番椒栽培品種。五個馴化種中除了*C. pubescens* 有黑色種子，*C. baccatum* 花冠基部有散漫黃斑，較易辨認外；其餘 *C. annuum*、*C. chinense* 及 *C. frutenscens* 三者則不容易自植株上花器或果實特性加以分類，必須以染色體鏡檢，或進行雜交親合力鑑定等方式，才能清楚的鑑別不同馴化種。

爲深入探討番椒演化過程中種間遺傳相似性（similarity），評估地域性種原演化歧異度，或鑑別新野生種原之血緣，近五年來國際間多位學者已著手研究應用鑑別能力較敏銳且快速的分子生物標誌，作爲番椒種原遺傳分析。如 Conicella（1989）以酯酵素（esterase）之同功異構酵素，探討不同地域來源之番椒（*Capsicum annuum* L.）種原[2]，結果以 esterase 酵素圖譜分爲 A、B、C 三型，種原來自美國南部者依不同區可分屬 A、B 二型；墨西哥地全屬 A 型；中美洲全屬 B 型；南美洲的秘魯 B 型；哥倫比亞 C 型，此結果可用以評估種原蒐集地點的歧異度，提供育種人員之參考。Inai 等人（1993）利用 RAPD marker，進行甜椒 *C. annuum* 與辣椒*C. chinense* 種間雜交之後裔中矮化遺傳基因的篩檢[5]。Prince 等人（1995）利用RAPD 分析21個源自不同地區之不同種的番椒品系，結果除發現 PCR 反應產生的多型性 DNA 片段，可清楚的作爲品種間 DNA 指紋比對（DNA fingerprinting）外，這些 PCR 增殖的 DNA 多型性片段，經 UPGMA 的群集分析（cluster analysis），可清楚的將21品系分成四群，其中 *C. annuum* 與 *C. frutescens*遺傳相似性最高，但與 *C. baccatum* 的遺傳相似性較小[11]。

本省位於番椒主產區的亞洲地帶，故亞洲蔬菜研究發展中心（Asian Vegetable Research & Development Center, AVRDC）多年來針對此一重要蔬菜，積極自世界各地進行種原蒐集與保存，目前該中心內番椒種原已達4,000品系以上。而本省爲因應種原保育與利用對未來國際間農業上之重要性，特於1993年在臺灣省農業試驗所內成立國家作物種原中心，負責本省之作物種原之蒐集與保存，對番椒此一重要蔬菜作物已逐年備份保存至種原庫內，目前入庫之番椒種原已達1,000品系以上。本研究目的即自其中取得部分代表性種原，期以快速有效的 RAPD 分析方式，建立不同「種」之分類標誌。藉由分子標誌之建立，配合遺傳相似性群集分析，達到更詳實之種原鑑別與管理。俾對於新蒐集或引進種原親緣鑑別與地域性種原歧異度的評估有所助益，提高遺傳資源應用之正確性。

材料與方法

一、植物材料

取自亞洲蔬菜研究發展中心蒐集番椒屬（*Capsicum*）14個品系，源自日本、美國、巴西和匈牙利等地區（Table 1），包含 *C. annuum*，*C. baccatum* 及 *C. chinense*，等三個經濟栽培之馴化種。其中除 *C. annuum* 內的 C01125、C01238、C01127 爲甜椒外，其餘均爲辣椒。供試14品系的番椒種子於1995年 9 月播種，一個月育苗後定植於 9 吋素燒盆，種植於玻璃溫室內。栽培介質係以 Bio-Mix TTING SOIL 2 混合粗發泡煉石（3：1）種植，至1996年一月至二月之結果期，參考

AVRDC番椒性狀調查，記錄未熟果色、成熟果色、果長、果實、果重及果形等果實性狀。

表 1. 進行種間多型性研究之番椒種原代號與基本資料
Table 1. Accessions of pepper (*Capsicum* spp.) used in the interspecific polymorphism study.

Order number	P.I. no.	Species	Country of origin	Cultivar
1	HC0001	*C. annuum*	USA	Hungarina yellow
2	HC0002	*C. annuum*	USA	Jaiapene
3	C01454	*C. annuum*	Japan	Goshiki
4	C01665	*C. annuum*	Zambia	
5	C04701	*C. chinense*	Brazil	
6	C04073	*C. baccatum*	Brazil	
7	C02090	*C. annuum*	Hungary	Cseresznyepaprika
8	C04676	*C. chinense*	Brazil	
9	C04191	*C. baccatum*	Brazil	Pimenta
10	C04164A	*C. baccatum*	Brazil	Pimenta
11	C00196-1	*C. annuum*	USA	
12	C01125	*C. annuum*	USA	Yelllow Oshkosh
13	C01238	*C. annuum*	Switzerland	Piment de Genesa corer de boaf
14	C01127	*C. annuum*	Romania	Arolei Lung

二、DNA 萃取

取植株嫩葉0.15公克放入1.5ml已滅菌的小離心管，加入液態氮磨碎，後加入500μl的 DNA 萃取緩衝液（100mM Tris-HCl，pH8.0；20mM EDTA；1.4mM NaCl；0.2%(v/v)β-mercaptoethanol），再放入65°C水浴30分鐘，輕輕混勻後加入500μl chloroform-isoamyl alcohol（24：1，v/v）再輕輕混勻。，以20°C，16,000g離10分鐘（SIGMA 2K15，rotor 12145）。再取上清液加入300 μl之冰冷 isopropanol，混合均勻後放置在室溫下沉澱1～2小時（或－20°C，隔夜）。再於4°C，16,000g離心10分鐘。小心倒掉上清液，再加入1ml的 washing buffer（76% ethanol（v/v）；10 mM ammonium acetate）輕輕混勻後，再於4°C下以16,000g離心10分鐘。再倒掉上清液，將沉澱的 DNA置於無菌操作臺風乾。風乾的 DNA 溶於50μl的無菌水再加入 RNase（10μg/ml）在37°C下反應20分鐘。最後取10μl的 DNA 溶液，稀釋100倍並測定 OD260nm 之讀值，及計算DNA 含量濃度。

三、聚合酵素連鎖反應（Polymerase Chain Reaction, PCR）與電泳

將萃取得之 genomic DNA 先稀釋成5ng/μl放置在－20°C下，提供聚合酵素連鎖反應時，作爲模板 DNA（template DNA）。另外利用10個核甘酸序列的隨意引子300種（UBC RAPD primer set：100/4及100/5 200種；Operon KitA：AO、AP、AQ、AR、AS 100種），並由先前 PCR 反應產物中篩選出多型性 DNA 片段明顯的引子 6 個：UBC313，UBC327，UBC346，UBC441，UBC457，UBC484（王，1995）進行聚合酵素連鎖反應。反應時採用0.5ml已滅菌的小離心管進行，反應液參考 Oard 及 Dronavalli (1992)，反應總體積爲25μl，內含1 u *Taq* ploymerase (Promega)、1×PCR buffer（50mMKCl；10mM Tris-HCl，pH9.0；0.1% Triton 100）、2.5 mM $MgCl_2$、200μM dNTP、20μM primer 及 25ng template DNA。聚合酵素連鎖反應儀器爲 Perkin Elmer Cetus Thermal Cycler480，反應溫度條件參考 Oard 及 Dronavalli (1992)，設定

如下：1次（cycle）：94°C，3分鐘→37°C，1分鐘→72°C，1分鐘；44次（cycles）：94°C，1分鐘→37°C，1分鐘→72°C，2分鐘。反應完成時自動保存在4°C。

經聚合酵素連鎖反應而增殖之DNA，取12μl加入稀釋6倍的電泳緩衝液（6×loading buffer：0.25% bromophenol blue 及 xylene cyanol，40% w/v sucrose），以2%的 agarose 在 TAE buffer（40 mM Tris acetate，pH 8.0；1mM EDTA）中進行 DNA 電泳。電泳槽係採用 Cosmo 生產的 Mupid-2，電壓設定100伏特，電泳時間約25分鐘，結束後置於0.5mg/ml 的ethidium bromide 中染色20～30分鐘，再置於 UV 光箱中，檢視 agarose 膠體上DNA 多型性片段，並照相及貯存影像於 IS 500 Digital Imaging System（Alpha Innotech Corporation）進行分析。

四、資料分析

群集分析是採用 Gel-Compar 軟體，計算兩品系間所有分析的 RAPD 條帶中相同條帶的比率。所有樣品兩兩分析後以 UPGMA（Unweighted Pair-Grouping Method Using Arithmetic Averages）估算相似性程度。RAPD 產物的 DNA 片段係以ϕ174/HaeIII 作爲估算分子量。並以 Dice's 相似性係數製矩陣表格，相似性係數值的計算方式爲 $F=2nxy/nx+ny$。nx 及 ny 分別代表 X 及 Y 品系的所有多型性 DNA 片段，nxy 則表示 X 及 Y 品系間都共有的片段數（simple matching coefficient, Nei & Li 1979），再於 Digital 個人電腦中以 Gel-Compar 軟體進行 UPGMA 群體分析，估算品系間遺傳相似程度。

結　　果

一、果實性狀

來自不同地區的番椒屬內之不同馴化種（表1），其果實性狀（果形及果色等）明顯不同（圖1，表2），於結果期可依自果形區別不同種原。一般而言，甜椒品系的果型要較大於辣椒品系，相對果重也較大。參試品系中C01127、C01125及C01238三甜椒品系之果形明顯較大（表2）。供試14品系之未熟果色爲黃或綠色，成熟果色則有黃、橙紅、紅色；果形有尖長型、圓錐形、卵圓形、鐘形等。由不同果色與不同果形可初步瞭解番椒種原的歧異性之表現。

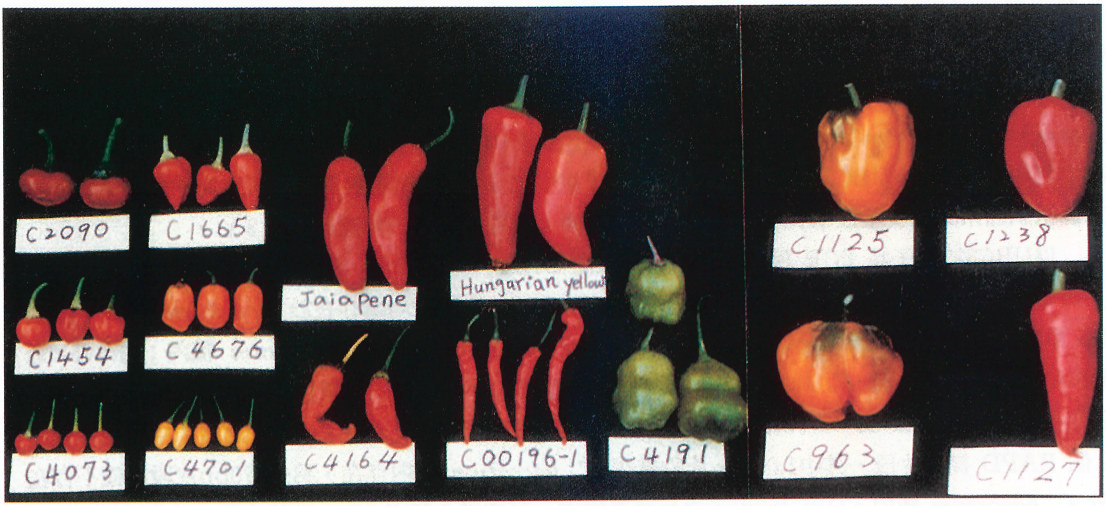

圖 1. 不同番椒馴化種之果實型態

Fig. 1. Fruit shapes of comesticated species of *Capsicum*.

表 2. 14個供試番椒種原之果實特性
Table 2. Fruit characterizations obatined from 14 accessions of pepper

P.I.no	Fruit color		Fruit size			Fruit shape
	Immature	Mature	Length (cm)	Width (cm)	Weight (g)	
HC0001	green	red	8.5	3.4	26.0	elongate
HC0002	green	red	7.2	1.8	13.1	elongate
C01454	yellow	orange-red	1.6	1.6	2.1	conical
C01665	yellow	red	2.6	1.8	2.7	conical
C04701	yellow	yellow	1.3	0.7	0.4	conical
C04073	green	red	1.1	1.0	0.64	round
C02090	green	red	2.4	2.8	9.0	oblate
C04676	green	orange	2.6	1.3	2.8	oval
C04191	green	red	4.0	3.1	14.0	campanulate
C04164A	green	red	5.1	1.6	4.0	elongate
C00196-1	green	red	4.9	0.7	1.0	elongate
C01125	green	yellow	7.5	5.2	52.1	bell
C01238	green	red	6.5	4.7	42.0	conical
C01127	green	red	10.1	3.1	31.0	conical

二、逢機增殖多型性 DNA 標誌

逢機引子300種（UBC RAPD primer set：100/4及100/5共200種；Operon Kit A：AO、AP、AQ、AR、AS共100種）經由先前 PCR 反應產物中所進行 RAPD 分析結果，篩選出多型性 DNA 片段表現明顯的引子 6 個：UBC313，UBC327，UBC346，UBC441，UBC457，UBC484[1]，以此 6 個篩選得到的引子，進行番椒屬新引進14個不同馴化種之 RAPD 分析。結果以UBC327（圖 2）、UBC346（圖 3）、UBC441（圖 4）及UBC457（圖 5）四個引子進行之 PCR 反應，在 *C. annuum*，*C. baccatum* 及 *C. chinenese* 三個馴化種間，均可產生清晰且具辨識效用之多型 DNA 片段；其中UBC327、UBC346及UBC457三個引子產生之 RAPD 圖譜更具有指紋比對之效果。由於在14個供試品系間之多型性 DNA 圖譜表現均不相同，可用於鑑別不同種原（表 3）。

以UBC327引子經 PCR 反應，所產生多型性 DNA 片段產物中，獲得 5 個可用於識別不同「種」的 DNA 片段（圖 2，表 4），其中2,749bp及1,348bp二片段均僅存在於 *C. chinense* 種內；942 bp DNA 片段僅在 *C. baccatum*種內存在；420bp片段只存在於 *C. annuum* 種內；另外652bp DNA 片段則不存在於 *C. baccatum* 種內。由 UBC346中獲得 2 個多型性 DNA 片段：1,353bp及260bp，可用於標誌 *C. baccatum*（圖 3，表 4）。由UBC441引子經 PCR 反應產物中，也可獲得 2 個 RAPD 標誌片段，其中1,069bp片段僅在 *C. baccatum* 種內存在，另外370bp片段則僅不存在於 *C. baccatum* 種內。UBC457引子之反應產物中，可獲得 2 個 RAPD 標誌片段，其中833bp片段不存在於*C. chinense* 種內，618bp片段則僅不存在於 *C. baccatum* 種內（圖 5，表 4）。

表 3. 以 RAPD 爲番椒馴化種鑑別之引子

Table 3. Rrimers used for RAPD analysis and discrimination of *Capsicum* domesticated species

Primer	Sequence
UBC327	5′ATACGGCGTC3′[z]
UBC346	5′TAGGCGAACG3′[z]
UBC441	5′CTGCGTTCTT3′
UBC457	5′CGACGCCCTG3′[z]

[z] Possessed fingerprinting effect.

表 4. 以 RAPD 特定分子片段之存在(+)或不存在(−)標誌番椒屬之不同種

Table 4. Presence(+)or abscence(−)of RAPD markers in genus of *Capsicum*.

Primer	Polymorphic DNA marker	*C. annuum*	*C. baccatum*	*C. chinense*
UBC327	2749bp			+
	1348bp			+
	942bp		+	
	625bp		−	
	420bp	+		
UBC346	1353bp		+	
	260bp		+	
UBC441	1061bp		+	
	370bp		−	
UBC457	833bp			−
	618bp		−	

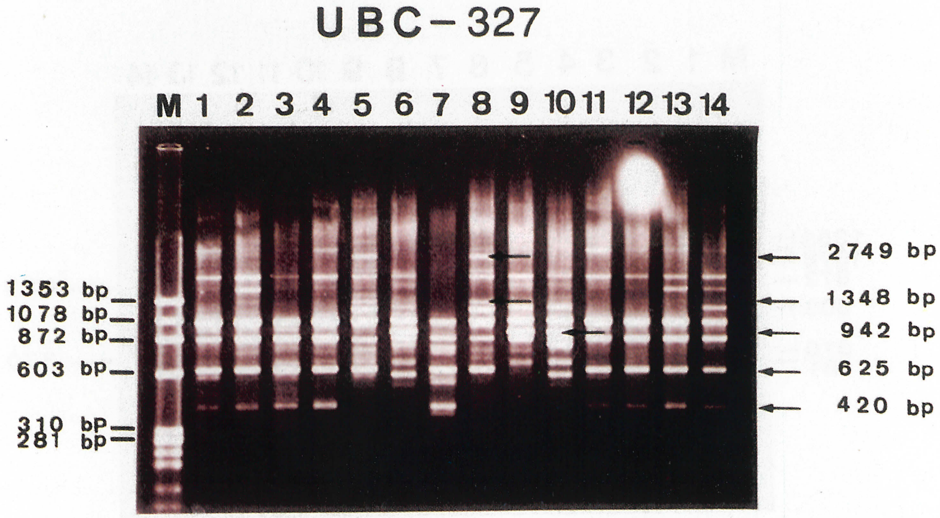

圖 2. 番椒屬14品系（如表 1），以UBC327爲引子之 RAPD 圖譜

Fig. 2. RAPD profiles generated by primer UBC-327, resolved by 2.0% agarose gel. Numbers on top refer to the accessions listed in Table 1.

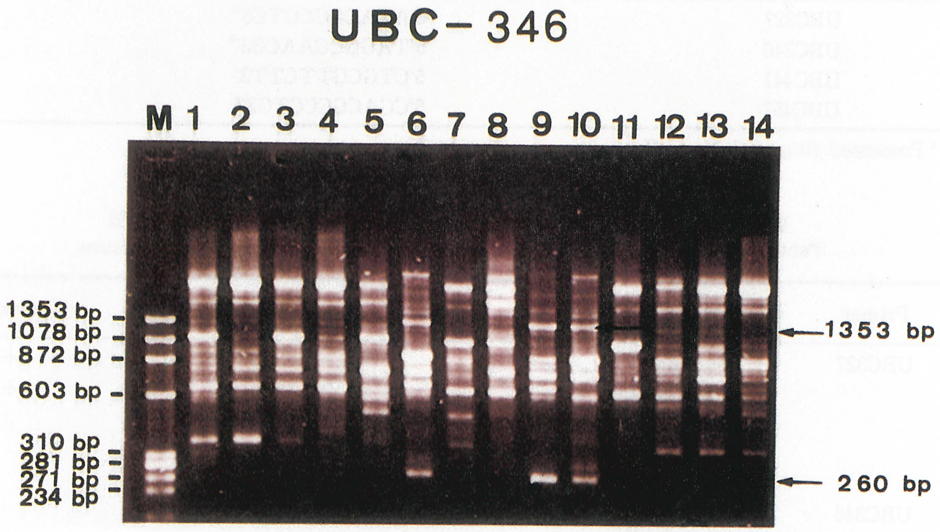

圖 3. 番椒屬14品系（如表 1），以UBC346爲引子之 RAPD 圖譜

Fig. 3. RAPD profiles generated by primer UBC-346, resolved by 2.0% agarose gel. Numbers on top refer to the accessions listed in Table1.

圖 4. 番椒屬14品系（如表 1），以UBC441爲引子之 RAPD 圖譜

Fig. 4. RAPD profiles generated by primer UBC-441, resolved by 2.0% agarose gel. Numbers on top refer to the accessions listed in Table1.

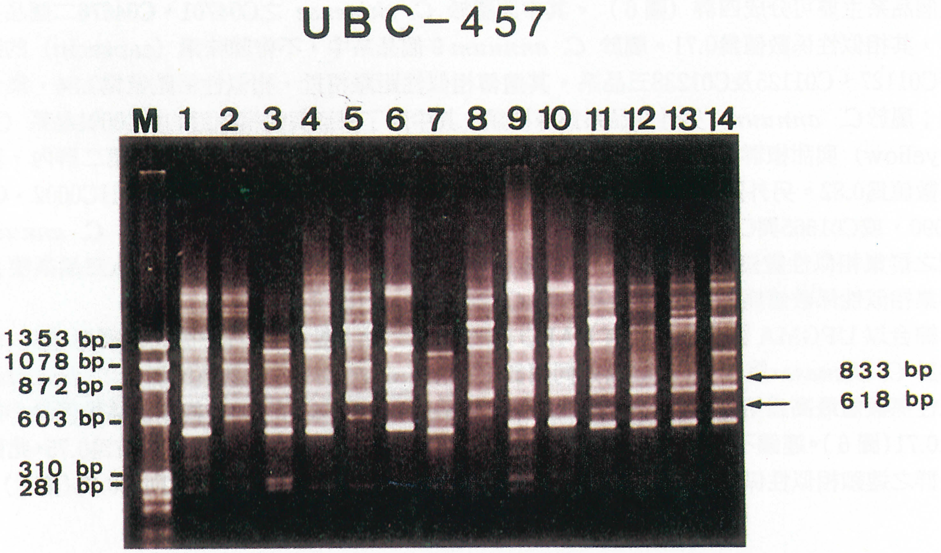

圖 5. 番椒屬14品系（如表1），以UBC457爲引子之 RAPD 圖譜

Fig. 5. RAPD profiles generated by primer UBC-457, resolved by 2.0% agarose gel. Numbers on top refer to the accessions listed in Table1.

將UBC327、UBC346、UBC441及UBC457四個引子，經 PCR 反應之所有 RAPD 多型性片段以 Dice's 相似性係數進行 UPGMA 群集分析。計算相似性係數(Dice's similarity coefficient)構築相似性矩陣(simliarity matrix)之結果顯示，供試的14個番椒品系之相似性係數值自0.5至1.0(表5)。相似性係數值最低的0.5，存在於C04701(*C. chinense*)與C04164A(*C. baccatum*)二品系間；相似性係數值最高之1.0，存在於C01454(*C. annuum*)與HC0002(*C. annuum*)二品系間(表5)。

表 5. 番椒14品系之 RAPD 圖譜，以 Dice's 計算之相似性矩陣

Table 5. Similarity matrix for Dice's coefficient among 14 pepper accessions

Accession no.	symbol	1	2	3	4	5	6	7	8	9	10	11	12	13	14
C04701	1	1.00													
C04676	2	0.71	1.00												
C01127	3	0.71	0.71	1.00											
C01125	4	0.63	0.63	0.82	1.00										
C01238	5	0.67	0.67	0.87	0.96	1.00									
HC0001	6	0.71	0.59	0.80	0.82	0.86	1.00								
C01665	7	0.71	0.71	0.59	0.74	0.78	0.71	1.00							
C00196-1	8	0.77	0.77	0.75	0.67	0.71	0.75	0.92	1.00						
HC0002	9	.071	0.71	0.71	0.74	0.78	0.85	0.86	0.92	1.00					
C01454	10	0.71	0.71	0.82	0.74	0.78	0.82	0.86	0.92	1.00	1.00				
C02090	11	0.80	0.67	0.89	0.70	.0.74	0.78	0.80	0.86	0.93	0.93	1.00			
C04073	12	0.53	0.67	0.67	0.70	0.63	0.56	0.87	0.71	0.53	0.53	0.63	1.00		
C04191	13	0.63	0.63	0.74	0.76	0.80	0.74	0.75	0.80	0.63	0.63	0.71	0.82	1.00	
C04164A	14	0.50	0.75	0.53	0.67	0.60	0.63	0.75	0.67	0.63	0.63	0.59	0.82	0.78	1.00^z

^{z} Range of value from 0 to 1.00, values closer to 1.00 indicating increasing similarity.

由 similarity matrix 繪製14個品系間 UPGMA 分析之群集樹狀圖（dendrogram）的結果顯示，14個品系主要可分成四群（圖 6）。其中原屬於 *C. chinense* 之C04701、C04676二個品系分在第一群，其相似性係數值爲0.71。屬於 *C. annuum* 9 個品系中，不帶辣味素（capsacin）的甜椒類，包含C01127、C01125及C01238三品系，其遺傳相似性距離相近，相似性係數值爲0.84，集合在第二群內；屬於*C. annuum* 另外 6 品系爲辣椒類，其中除了果形與甜椒相近的HC0001品系（Hungarian yellow）與甜椒群（C01127、C01125及C01238）遺傳距離較近，同集合在第二群內，群集相似性系數值爲0.82。另外同屬於 *C. annuum* 之辣椒類 5 品系集合成第三群，其中HC0002、C01454及C02090，或C01665與C00196-1相似性係值較高，分別爲0.93及0.92，總合第三群 *C. annuum* 的辣椒類之群集相似性數值爲0.75。最後第四群爲其餘的C04073、C04191、C04164A三品系集合成一群，群集相似性係數值爲0.8，此三品系均爲 *C. baccatum*（圖 6）

綜合以 UPGMA 群集分析所有 RAPD 產物獲得之樹狀圖，結果可分成的四群中，第一群之品系同屬於 *C. chenese*，第二、三群之品系同屬於 *C. annuum*，第四群之品系同屬於 *C. baccatum*。群內相似性係數值最高爲第三群之0.87，其次爲第二群的0.82及第四群的0.80，相似性係數值最小的是第一群之0.71（圖 6）。連鎖不同群間遺傳距離最近的是第二及第三群，其相似性係數值爲0.75，此兩群再與第一群之連鎖相似性係數爲0.70，上述一、二、三群與第四群之連鎖相似性係數則爲0.65（圖 6）。

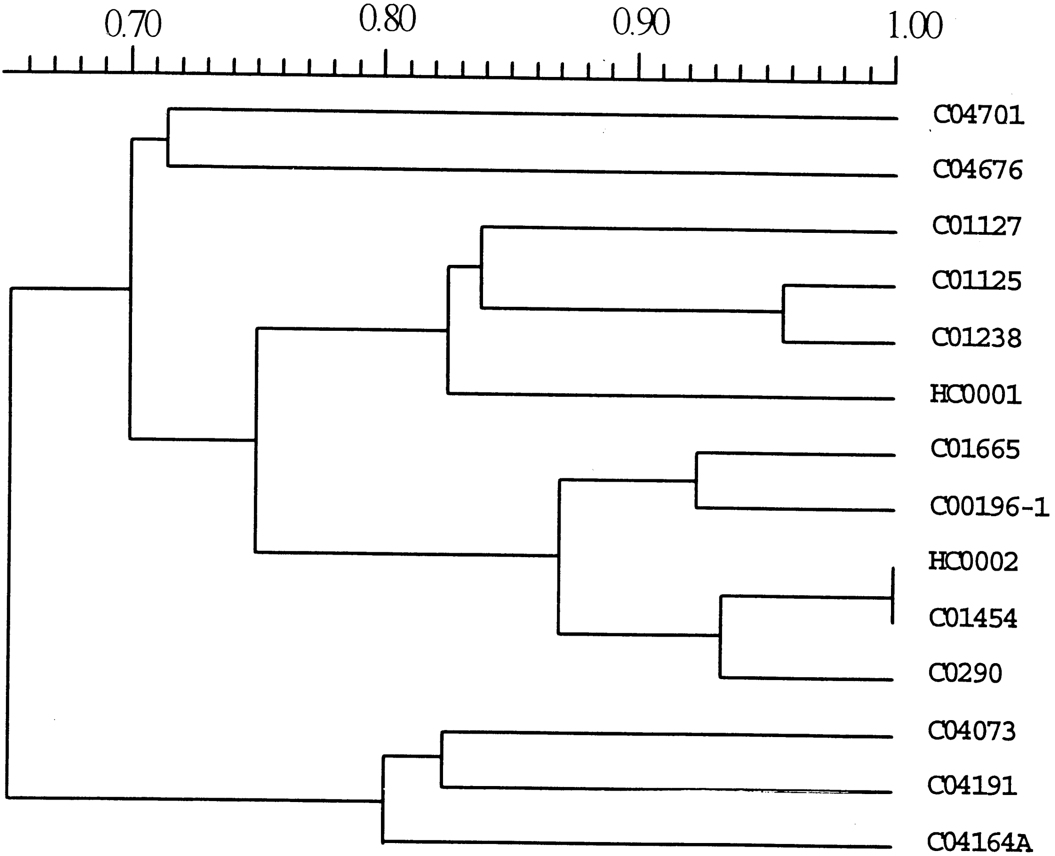

圖 6. 番椒14品系之 RAPD 圖譜，經 Dice's 計算之相似性矩陣所構築之相似性樹狀圖

Fig. 6. Dendrogram of 14 pepper accessions, constructed by UPGMA based on Dice's similarity coefficients. The scale on the top is Dice's coefficient of similarity.

討　論

早期最傳統的植物分類方式，不外乎利用一些植物外表型態或性狀（如花器、果實等）進行分類或「種」的鑑別，這種分類方式在番椒作物上也不例外。Pickergill 等人（1969）以花器及果實特性等植物性狀，可分辨番椒屬（*Capsicum*）中的五個馴化種：*C. baccatum*、*C. pubescens*、*C. annuum*、*C. chinense* 及 *C. frutsecesns*，但後三個「種」間植物性狀相似性較高，有時並不容易完全區分。McLeed 等人（1983）進一步利用同功異構酵素分析番椒種原，使番椒種間之分類除植物性狀外，進入分子生物鑑別的層次。以酵素電泳分析除了證實番椒可分爲五個馴化種外，由其酵素圖譜（zymogram）表現，另可證實 *C. annuum*、*C. chinense*及 *C. frutescens* 三個種具有很高的相似性。其後，Prince 等人（1995）利用RAPD 分析不同來源地區之番椒種原，發現 *C. annuum*，*C. frutescens* 及 *C. baccatum* 三個馴化種的各不同品系經群集分析結果，屬於同一馴化種的品系，可自然集合成一群，此對於「種」的分析具有高效的鑑別能力；此外對於同「種」內的不同品系以 RAPD 分析也能達到指紋比對的效用。另外，王（1995）同樣以 RAPD 分子標誌用於番椒品種鑑定時發現，RAPD分析可用於 *C. annuuum* 種內不同栽培或雜交種之鑑別，且利用這些 RAPD 分析之多型性DNA 片段，經 UPGMA 群集分析，也可正確的評估品系間遺傳親緣的相似性，並與植物性狀分類結果吻合。

本研究延續過去以 RAPD 分子標誌用於番椒品種鑑定所篩選得之引子，並擴展研究材料包含源自日本、美國、巴西和匈牙利等地區之*C. annuum*，*C. chinense* 及 *C.baccatum*三個馴化種間之品種爲材料，結果發現，這些品系經進行 RAPD 標誌及群集分析，也會將屬於同一馴化種的品系集合成一群。因此利用 RAPD 分析技術，可將演化上相似性高的馴化種歸成遺傳距離相近的一群（圖 6），對於「種」的演化或分類，應爲一種有效的證明或鑑定工具。

本試驗印證 RAPD 之分析，可以正確的提供種間或種內遺傳相似性，評估種原歧異度或不同品系間遺傳上血緣相似性；此外藉由 RAPD 分析所篩選得到具明顯多型性的特定引子，經 PCR 反應後，自產物中另可得到具有不同「種」間相異且特有的 DNA 片段之存在。如本研究中，引子UBC327經 PCR 反應，產物中2,749bp及1,348bp二個增殖的 DNA 片段都可以作爲鑑別 *C. chinense* 的特有條帶（圖 2，表 4）；942bp片段可以作爲鑑別 *C. baccatum* 的特有條帶（圖 2，表 4）；420bp片段則可作爲鑑別*C. annuum* 的特有條帶（圖 2，表 4），故以引子UBC327進行PCR 反應，即可篩檢出番椒屬內 *C. annuum*、*C. chinense* 或 *C. baccatum* 三個不同「種」之種原，此對於新蒐集引進及血緣不清楚之野生種原鑑定上，即可在幼苗階段萃取其genomic DNA 進行 RAPD 分析而得知應屬於何「種」，或評估與某些已知重要種原之血緣相關性，此除了具有快速且正確鑑別種原的目的外，對於提高種原保育與利用效率也具正面價值。

以 RAPD 進行種原分析時，另一個值得注意的問題是，作物的授粉行爲與基因同質性高低等遺傳特性。自花授粉（self-pollinationing）作物如茄科的番茄，其 DNA 多型性表現會較低，而異花授粉的作物如玉米，進行 RAPD 分析時則容易表現較高的多型性（Helentjaris, et. al, 1986）。另外遺傳基因同質性的高低也與 RAPD 分析樣品取樣數目之大小具關連性。同質性低的作物要取得一定數目的樣品（株），混合後萃取其 genomic DNA，才具有該種質（germplasm）的代表性。Yang 等人（1993）以芹菜爲例，建議最好混合5～20株的樣品，萃取其 genomic DNA，作爲 PCR 反應中的模板 DNA，才具有代表性。其餘不同作物則應視其基因同質性高低，考慮模板 DNA萃取時使用植株取樣之多寡，才能使該 genomic DNA 具代表性，隨之進行 PCR 反應，其 RAPD 分析之產物才能有更正確之判讀數值。本試驗材料番椒爲常異交作物，而目前係採 3 株之材料混合代表，未來將再就遺傳特性對 RAPD 分析之再現性，與取樣品數目之相關性，作進一步之探討。

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Study on the Molecular Markers of *Capiscum* Wild/Domesticated Species Using Random Amplified Polymorphic DNA Analysis[1]

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Summary

Fourteen pepper (*Capsicum* spp.) accessions, originated from Japan, USA, Brazil, and Hungary etc. were surveyed by random amplified ploymorphic DNA (RAPD) analysis. The results indicated that high degree of polymorphism was obtained from four random decamer primers (UBC327, UBC346, UBC441, and UBC457) which produced 11 reproducible and effective amplification fragments useful for identification between species. Besides, each of the tested accessions of *Capsicum* could be exactly distinguished from each other by using the primers of UBC327, UBC346, and UBC457. Results of smilarity analysis cluster analysis (UPGMA, Unweighted Pair-Grouping Mean Arithmetic Averages) revealed these accessions could be divided into four groups : the first contained 2 accesssions, belonging to *C. chinense,* the second was composed of 4 accessions, belonging to *C. annuum,* the third contained 5 accessions, also belonging to *C. annuum,* and the fourth had 3 accessions, belonging to *C. baccatum.* The results strongly suggested that RAPD markers possessed the effect of fingerprintig and could be effectively and reliably used for classification *Capsicum* spp..

Key words : Random amplified polymorphic DNA (RAPD) , Cluster analysis, DNA fingerprinting, Pepper (*Capsicum* spp.)

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杏鮑菇稻草栽培之研究 [1]

彭 金 騰 [2]

摘要：風乾稻草經切短爲一吋左右，加足水份並塡加以稻草乾重1%之氫氧化鈣，在不塡加任何營養之情形下堆積20天後，裝袋並以95至100°C水煮6小時處理，可做爲杏鮑菇（*Pleurotus eryngii*）之栽培基質。經以上處理，3公斤含水量約爲70%之稻草，分別接種 ATCC36047 及 CCRC 36037兩杏鮑菇菌株，在17～18°C之栽培溫度下，30天內之平均產量依次爲425.0及137.5g，其差異達1%之顯著水準。又若稻草經加水堆積2個月後，方以95～100°C分別水煮2，4或6小時，則3公斤含水量約爲68%之以上3種處理的稻草，接種 ATCC 36047 杏鮑菇菌株，亦在17～18°C之栽培溫度下，35天內之平均產量依次爲346.7，382.5及170.0g。水煮時間爲6小時之處理的稻草基質因受木黴感染，導致產量降低。

關鍵詞：杏鮑菇、稻草、栽培。

杏鮑菇〔*Pleurotus eryngii*（DC.：Fr.）Quél.〕是屬於亞熱及草原地帶之典型菇類，分佈於歐洲，中亞及北美地區。俄國人 Vasilkov 稱之爲草原的美味牛肝菌（the boletus of steppes）[5]，Singer 評爲所有蠔菇屬中最佳的物種[3]，其菌柄及菌傘之質地，風味及烹調特性比任何其它鮑魚菇類爲佳，是非常值得開發之高品質食用菇[7]。此菇在全世界鮮有商業化栽培，其困難在於其菌絲生長緩慢及對其他微生物之抵抗性太弱之緣故[7]。杏鮑菇在義大利已有少量商業化栽培，係採用經高溫殺菌處理之麥桿爲材料[4]，惟本省麥桿不多卻有豐富的稻草，而迄今尙無以稻草栽培杏鮑菇之報告發表，本研究之目的在於探討以稻草栽培杏鮑菇之可行性。根據 Caileux 與 Diop[1]之研究，杏鮑菇之菌絲生長溫度範圍爲20～30°C，最適溫度爲25°C，出菇適宜溫度範圍爲12～26°C，菇體發育最適溫度爲20～22°C，子實體正常發育所須之二氧化碳濃度爲 800ppm 以下，相對溼度爲80～85%，光線爲5～400lux，基質酸鹼度爲 pH5～6，本研究根據以上杏鮑菇之基本生理特性，進行其稻草栽培之研究。

材料與方法

一、供試杏鮑菇品系：本研究所用之杏鮑菇品系包括自美國引進的 ATCC36047（美國菌種保存中心鍾順昌博士贈送）及自葡萄牙引進之 CCRC36037（葡萄牙 J.Sobral 贈送）兩菌株，均以馬鈴薯葡萄糖洋菜培養基做定期培養，並以液氮做長久保存。

二、供試菌種及栽培材料：本研究所使用之菌種採用小麥爲原料，栽培基質則以稻草爲主要材料。

三、小麥菌種之製作：小麥先以水洗淨並以冷水煮至沸騰，保持約20分鐘，濾除水分後，隨即塡加1%碳酸鈣，冷卻後裝入四角瓶，塞好棉塞以高壓蒸氣殺菌（121°C，1小時），隔夜冷卻後以上述兩杏鮑菇品系培養於 PDA 之菌絲塊接種，定溫培養於 25°C 約15天，當菌絲長滿小麥後即得

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小麥菌種。

四、第一次稻草栽培基質之製作及栽培：風乾稻草以切草機切短爲約 1 吋左右，隨即加水及添加稻草乾重1%之氫氧化鈣，經堆積20天，其間翻堆一次，然後裝入白色飼料袋，每袋約30公斤，並移入大型長方形聚乙烯塑膠桶（長 2 公尺，寬 1 公尺），每桶共置 7 至 8 袋，其上放置兩塊木板，並覆以水泥磚防上桶內加水後漂浮。當以自來水加至覆蓋稻草袋並將蒸氣輸管插入桶近中央處後，通入來自鍋鑪之蒸氣，待桶內之水溫達95～100°C時保持 6 小時。然後將熱水排掉，取出稻草袋，置於鐵網上，隔夜冷卻後，在較乾淨之處，以手扭乾稻草水份，秤好每份 3 公斤之稻草（含水量約70%）與半個四角瓶之杏鮑菇小麥菌種（約50公克）均勻混合後，裝入底部有打小孔（直徑0.5公分）之黑色聚乙烯塑膠袋（表面積203.7cm^2），經於21～23°C，走菌 1 個月後，覆以水苔泥炭土（Jourbesol, St. Raphael Peat Moss Ltd. Haut-Lameque, N.B. Canada）與紅土之混合物（體積比＝1：5），並移入兩栽培室，分別降溫至18～19°C及17～18°C，ATCC36047 菌株 在兩栽培室各有 8 袋，每袋一重覆，而 CCRC36037 菌株則僅於17～18°C之栽培室放置 8 袋，所有稻草袋均放置於第二層菇架上（距地面約80公分）。每間栽培室在降溫後，每日將室內地板以水沖溼，使室內相對溼度保持在85～90%，覆土表面亦須適量灑水，室內以日光燈照明（光度約200lux），待菇體形成，而菌傘尚未上翻前採收計重。

五、第二次稻草栽培基質之製作及栽培：風乾稻草以切草機切短爲約 1 吋長，並加水及添加乾稻草重量1%之氫氧化鈣，經戶外堆積約兩個月，其間每隔15天翻堆一次，然後依第一次之稻草栽培基質製作法，分別以95～100°C熱水處理 2、4 或 6 小時後取出稻草袋置於鐵網之上，隔夜冷卻後取出稻草，以脫水機去除多餘水分，並秤取每份 3 公斤之稻草（含水量約68%），經與供試杏鮑菇ATCC36047菌株之小麥菌種（約50公克）混合後，裝入底部有打小孔之黑色聚乙烯塑膠袋（表面積203.7cm^2），隨即移入21～23°C培養室菇架上，其上覆以白報紙，培養30天後，菌絲已長滿培養基質時，取下白報紙，覆以紅土，每處理各 8 袋，逢機排列於栽培室上下兩層之床架上，同時也將室內溫度降至17～18°C，每日將栽培室地板灑濕，早晚各一次，覆土表面亦予適量灑水，以日光燈照明，光度約200lux。菇體形成後，在菌傘尚未上翻前，採收並計重。

結果與討論

一、杏鮑菇第一次稻草栽培：本研究之目的在初步瞭解以純稻草是否可栽培杏鮑菇及栽培出菇期間之溫度對產量之影響，以及在同一溫度下不同杏鮑菇菌株之產量差異。經本研究結果顯示，儘管其產量是否合乎經濟尚待檢討，純稻草經堆積及水煮後，不須塡加任何其他營養確可栽培杏鮑菇（表 1），此與以麥桿爲主要材料做爲蠔菇或其他蠔菇屬菇類栽培基質之情形相似。蠔菇類物種屬於腐生菌，是主要的分解者，它具有直接分解含纖維素與木質素物質之能力，而所需基質不需要靠化學或生物性的特別處理製作，例如醱酵的過程[7]。洋菇合成堆肥含有相當高量之氮素，已證明不適於蠔菇類之栽培[2]。蠔菇類之栽培基質是不需要經過醱酵的，相反地，經醱酵處理後，反而會造成有機物之損失。因此蠔菇類之栽培基質，只要直接以100或80°C處理，經冷卻後即可接種，而此法可應用於機械化與連續性的基質製作，蠔菇類物種之菌絲在此種基質之生長與經高溫殺菌之基質並無區別[7]。本試驗結果顯示稻草經切短堆積水煮後，應可取代麥桿栽培杏鮑菇。根據 Zadražil 氏以麥桿栽培杏鮑菇時，所採收之菇體乾重量約爲原來麥桿乾重之10%[7]，以本試驗之產量計算尚未達到此標準，將來如何以機械化及自動化來製作稻草基質，並改進基質配方與栽培之環境條件，以達到經濟栽培之目的，是今後值得研究之主題。

栽培溫度對杏鮑菇產量之影響方面，本研究結果顯示栽培溫度控制於17至18°C時之產量較於18至19°C時爲高，且已達1%之顯著水準（表 1），但根據 Cailleux and Diop 兩氏[1]，杏鮑菇之出菇溫度爲12至26°C，最適溫度範圍爲20至22°C，本試驗結果顯示與此報告有所出入，此可能

與所栽培之品系或菌株不同所致。又在同一栽培溫度下，杏鮑菇 ATCC36047 菌株之產量較CCRC36037菌株為高（表２），且達1%之顯著水準，顯然不同杏鮑菇品系或菌株間有產菇力差異，此可為杏鮑菇選種或育種之參考。

表1.　栽培出菇期間之室內溫度對杏鮑菇稻草栽培產量之影響

Table 1. The effect of cropping temperature on the yield of *Pleurotus eryngii* grown on rice straw substrate[z].

Temperature	Yield(g/bag)[y]								Average[x]
	1	2	3	4	5	6	7	8	
18～19°C	375	395	365	320	360	315	300	320	342.8
17～18°C	440	390	385	470	405	520	410	380	425.0

[z]Air-dried rice straw was cut into pieces about 1 inch in length and watered sufficiently, followed by adding calcium hydroxide and heaped for 20days. The straw was then filled into minutely perforated plastic bags and soaked in boiling water for 6 hrs. After cooling down, the straw was squeezed with hand to remove excessive water. Theree kg of the obtained straw was mixed with wheat grain spawn (about 50g) and filled into a black polyethylene bag. Each has a bed surface of 203cm^2. After spawn running through the substrate, the surface was cased with a mixture of 1 part of peat moss with 5 parts of soil by volume.

[y]The relative humidity of the cropping room was maintained at 85～90% with a light intensity of 200lux. The cropping duration was 35 days.

[x]L. S. D. $_{0.05}$=45.3 L. S. D. $_{0.01}$=62.8.

表2.　不同菌株對杏鮑菇稻草栽培產量之影響

Table 2. Comparison of productivity between the two strains of *Pleurotus eryngii* grown on rice straw[z].

Strain	Yield(g/bag)[y]								Average[x]
	1	2	3	4	5	6	7	8	
ATCC 36047	440	390	385	470	405	520	410	380	425.0
CCRC 36037	150	195	180	100	180	115	85	90	137.5

[z]The substrate was prepared and cased as described in Table 1.

[y]The cropping condition was maintained at 85～90% in relative humidity, under 200lux light intensity, and 17～18°C in temperature. The cropping duration was 35 days.

[x]L. S. D. $_{0.05}$=50.4 L. S. D. $_{0.01}$=69.9.

二、杏鮑菇第二次稻草栽培：本研究之目的在瞭解以稻草為基質栽培杏鮑菇時，稻草水煮時間對產量之影響。研究結果顯示稻草經堆積兩個月後，方予水煮消毒時，如果處理時間達６小時，且下種後並以白報紙覆蓋較易受木黴（*Trichoderma* spp.）感染，而出菇期間仍繼續會受木黴之侵害，造成杏鮑菇菌絲之消失，嚴重影響產量。根據觀察，下種後初期，杏鮑菇菌絲生長頗為正常，後期則常有木黴侵害，此是否因覆蓋白報紙造成杏鮑菇菌絲產生之特有氣體不易排除，因而誘發木黴孢子之發芽及其後之菌絲發育，造成杏鮑菇菌絲之受害消失，尚待檢討，惟水煮時間若為２至４小時，則木黴之發生較少，而此二種處理之產量均較６小時之處理為高（表３），且已達1%之顯著水準，但２與４小時之兩種處理間，則無產量之顯著差異（表３）。本試驗研究第一次稻草栽培時，水煮消毒時間亦為６小時，但未見木黴之嚴重侵害，不過其稻草堆積時間僅二十天，因此稻草堆積時間之長短，似與木黴之發生有關，因而影響杏鮑菇之產量。此可能因為稻草堆積時間較長時，因醱酵所釋出之營養物質較多，導致木黴之容易發生，而堆積較長之稻草，水煮時間較長時，可能因基質之變化適於木黴之生長而增加木黴之感染機會，導致杏鮑菇產量之降低。

杏鮑菇以稻草栽培經本研究結果證明確可成功產生正常發育之菇體，惟若以所使用之基質重

量計，尚未達到一般蠔菇類應有之產菇潛力，本研究爲避免稻草水煮處理後之雜菌感染，已過濾可溶性養分，且未填加任何有機營養料，將來如能發展使用不易爲雜菌利用，經特殊處理之有機填加物或改進稻草堆積與殺菌之方法，產量應有再提高之可能。稻草經短期堆積軟化後，如何利用機械做連續性的加溫消毒，冷卻及菌種自動混合與裝袋，以減少雜菌污染，增加產量，節省人力，是今後值得研究之主題。

表3. 稻草栽培基質水煮時間對杏鮑菇產量之影響

Table 3. The effect of heat treatment of the rice straw substrate on the productivity of *Pleurotus eryngii*[z].

Heat treatment time (hrs)	Yield (g/bag)[y]						Average[x]
	1	2	3	4	5	6	
6	220	180	170	120	120	210	170.0 b
4	445	405	450	340	330	325	382.5 a
2	480	405	320	365	260	250	346.7 a

[z] Air dried rice straw was treated with the similar method as described in Table 1, except the heaping duration was 2 months and the perforated plastic bags containing straw was soaked in boiling water for 2, 4 or 6 hrs. After cooling down, the straw was centrifuged at low speed to remove excessive water. Three kg of the obtained straw (water content about 70%) was mixed with wheat grain spawn (about 50g) and filled into each black polyethylene bag. The bed surface of each bag was 203cm^2. After spawn runing through the substrate, the surface was cased as described in Table 1.

[y] The cropping condition was maintained at 85～90% in relative humidity, under 200 lux in light intensity, and 17～18°C in temperature. The cropping duration was 35 days.

[x] Means with the same letter of a column are not significantly different at 5% level by Duncan's multiple range test.

圖 1. 杏鮑菇 ATCC36047 菌株在稻草基質（稻草堆積20天，95～100°C熱水處理 6 小時）之出菇情形

Fig. 1. Fruitbodies of the strain ATCC 36047 of *Pleurotus eryngii* grown on rice straw which had been heaped for 20 days and soaked in boiling water for 6 hours.

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The Cultivation of *Pleurotus eryngii* (DC. : Fr.) Quél. on Rice Straw Substrate[1]

Jin-Torng Peng[2]

Summary

Air-dried rice straw was cut into short pieces about 1inch in length and watered sufficiently. After being added with calcium hydroxide, the straw was heaped for 20 days without adding any other nutrient. The straw was then filled into minutely perforated plastic bags and soaked in boiling water for 6 hrs. The resulted substrate was found to be able to grow *Pleurotus eryngii*. After spawning and spawn running, 3kg of this straw containing 70% of warer could produce 425.0 g and 137.5 g of fruitbodies for the strain ATCC 36047 and CCRC 36037, respectively, in 35 days when cropped at 17~18°C. If the rice straw was heaped for 2 months followed by soaking in boiling water for 2, 4, or 6 hrs, 3kg of the treated straw containing 68% of water could produce, respectively, 346.7 g, 382.5, and 170.0 g of fruitbodies in 35 days when cropped at 17~18°C. The treatment of 6 hrs' soaking in boiling water resulted in much less fruitbody yield because the straw was severely infected by *Trichoderma* spp. after the mushroom mycelium had grown throughout the substrate.

Key words : *Pleurotus eryngii*, Cultivation, Rice straw.

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杏鮑菇木屑塑膠包栽培之初步研究[1]

彭 金 騰[2]

摘要：雜木木屑（主要爲山黃麻與楓木）添加20%（體積）之米糠，經加水混合均勻裝入聚丙烯塑膠袋予以高壓蒸氣殺菌後製備之基質，經接種走菌並於17至18°C，在有照明及相對溼度爲95%以上之條件下栽培結果顯示，可以取代麥桿或稻草栽培杏鮑菇。接種至出菇約須60天，在45天採收期內，含1.2kg基質（水分含量約60%）之塑膠培養包，當豎放未割包時，每包之平均產量約101 g，所產生之菇體大，傘肉厚，菇柄直而粗，外形佳。而當培養包橫放且在包底割十字切口時，每包平均產量約154 g，菇體較小，傘肉薄，菇柄彎曲而細，外形較差。

關鍵詞：杏鮑菇、木屑、塑膠包、栽培。

杏鮑菇〔*Pleruotus eryngii* (DC.: Fr.) Quél〕爲一高品質食用菇(1,4,6)，可以麥桿或稻草爲主要材料，經80至100°C熱處理後栽培(2,3,5,6)，但因其菌絲生長較慢且對其他微生物之抵抗性甚弱(2)，而栽培基質並未完全殺菌，且下種之後即暴露空氣中，在菌種走菌及栽培期間易受雜菌污染或病原菌侵害(2)，因此迄今鮮有商業化生產(2,6)。本研究之目的在於初步探討以木屑取代麥桿或稻草，經添加營養物後，以高壓蒸氣殺菌而非低溫或半高溫殺菌處理後栽培杏鮑菇之可行性及木屑塑膠培養包放置方法對杏鮑菇產量及菇體外觀品質之影響。

材料與方法

一、供試杏鮑菇菌株：本試驗所使用之杏鮑菇菌株爲 ATCC 36047，係美國菌種保存中心鍾順昌博士所贈送，以馬鈴薯葡萄糖洋菜培養基做定期培養，並以液氮做長久保存。

三、供試菌種之製作：本研究供接種之菌種的製作方法，請參考彭氏 (1996)(2)。

四、木屑塑膠包之製作及接種：新鮮雜木（主要爲山黃麻及楓樹）木屑，自鋸木廠購得後，經堆積戶外四個月後使用，其間須灑水並每隔一個月翻堆一次。經堆積過之木屑以電動篩選機去除木屑內之木塊、細枝條及其他雜物後，加入20%（體積）米糠及適量碳酸鈣，將木屑米糠混合物之pH 值調整於約6.5，經適量加水，以電動混合機（建泉牌）混合均勻（含水量約60%）後，以半自動裝包壓包機（忠興牌）製作木屑塑膠包（聚丙烯耐熱透明塑膠袋），每包重約1.2公斤，經套上聚丙烯塑膠製之頸環，並塞好棉塞，以高壓蒸氣殺菌（121°C，2小時），待隔夜冷卻後，以事先製妥之杏鮑菇小麥菌種接種，並移入室溫爲21～23°C之培養室培養約45天，俟菌絲長滿栽培基質時，即可供出菇之用。

五、木屑塑膠包的出菇管理：菌絲已長滿之杏鮑菇木屑塑膠包經移入栽培室，並將室內溫度調節於15～17°C，拔除棉塞，以每 24 包爲一重複，共做 8 個重複，分豎放未割包及橫放割包兩處理，每

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種處理各有一半重複在荷蘭床架式菇床之第一層及第二層上（第一層距地面30公分，第一與第二層菇床間相距50公分）。橫放時於塑膠包底部以利刃畫兩個十字，深約0.5公分。塑膠包移入栽培室並拔除棉塞後，每日將室內地面（水泥地）灑濕，但不直接將水灑於塑膠包之上，待菇體自頸口（直徑2.8公分）或割口處長出，且菌傘邊緣未上翻前採收，調查菇體形態並計重。

結果與討論

杏鮑菇木屑塑膠包經栽培結果顯示，當塑膠包橫放且割包時所形成之子實體，因有向光性，菇柄均爲彎曲，又因爲杏鮑菇之菇體生長習性屬叢生型，因此自割包處形成之菇體數目較多，多屬小型，傘肉較薄，菌柄多側生或偏生，菇體外觀較差（圖1），而自頸口處長出者因塑膠包底部亦有子實體之形成生長，可能因營養一時間供應不足，子實體個體較小。當塑膠包豎放未割包時，菇體均自塑膠包上面之頸口長出，雖因屬叢生型，若子實體之原基體不直接形成于近頸口處，而在頸口稍低處形成時，因空間受限，每頸口只有1至3個幼小菇體能發育成正常菇體，其餘均無法正常發育而枯萎乾燥。正常發育之菇體直立多呈淺漏斗形，菌柄多屬近中生，較粗大、傘肉較厚而外觀較佳（圖2）。惟自豎放之塑膠包頸口產生菇體較難且慢，形成之菇體較少，其總產量較橫放割包時爲低，並達1％之顯著水準（表1）。塑膠包橫放割包時，子實體可自頸口及割包處均可產生，所形成之菇體雖然較小但數量較多，在一定時間內對塑膠包內之營養利用之效率似較豎放未割包時爲高，因此其產量較後一處理爲佳。此外當塑膠包豎放時，頸口處可能因溼度保持較橫放時困難，導致出菇較不容易，或許亦是低產原因之一。

以上杏鮑菇木屑塑膠包栽培試驗結果顯示，利用雜木木屑與米糠之混合物，經裝包壓包以高壓蒸氣殺菌處理後，顯然可用以栽培杏鮑菇，且基質塑膠包之放置方法與割包與否對產生之子實體品質與產量均有影響，如何以基質材料配方之改善或栽培環境條件之改進以提高塑膠包豎放時之產量或促進均勻出菇及如何提高塑膠包橫放時之菇體品質與產量是今後杏鮑菇塑膠包栽培研究之重點。此外木屑塑膠包之栽培方式，由於栽培材料之裝填壓包及接種無法完全自動化且操作較笨重，如能改用金針菇瓶式栽培，則從栽培材料之混合至裝瓶及接種均可自動化，節省勞力成本，且採用空調栽培，生產不受氣候影響，是值得思考研究開發之方向。

表1. 木屑塑膠包橫放割包與豎放不割包對杏鮑菇產量之影響

Table 1. The effect of the direction of placing the sawdust bags during cultivation on the yield of *Pleurotus eryngii*[z].

Treatment	Fruitbody yield (g/24bags)[y]								Average[x]
	1	2	3	4	5	6	7	8	
Bags were horizontally laid with a cross fissure at bottom	4,170	3,665	3,575	3,330	3,290	4,090	4,130	3,270	3,690
Bags vertically placed without cutting	2,260	2,085	2,145	3,210	2,340	2,845	2,180	2,445	2,440

[z] The substrate in polypropylene bags was sterilized at 121°C for 2hrs. Each bag contained 1.2kg of substrate with a water content of about 60%.The diameter of the plastic ring on the top of the bag was 2.8cm.

[y] Each replicate had 24 bags. The cropping condition was maintained at>95% in relative humidity, 200 lux in light intensity, and 15~17°C in temperature. The cropping duration was 45 days.

[x] $L.S.D._{0.05}=414.9$，$L.S.D._{0.01}=575.8$。

圖1. 木屑塑膠包橫放且割包時之杏鮑菇出菇狀況

Fig. 1. Fruitbodies of *Pleurotus eryngii* produced on sawdust bags which were laid horizontally and a cross fissure was cut at the bottom of bag.

圖2. 木屑塑膠包豎放未割包時之杏鮑菇出菇狀況

Fig. 2. Fruitbodies of *Pleurotus eryngii* produced on sawdust bags which were placed vertically without cutting any holes on bags.

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Preliminary Studies on the Cultivation of *Pleurotus eryngii* (DC.: Fr.) Quél. on Sawdust Filled in Polypropylene Bags[1]

Jin-Torng Peng[2]

Summary

Sawdusts of broad leaved trees (mainly *Trema orientalis* and *Liquidambar formosana*) were mixed with 20% (by volume) of rice bran and watered. The mixture was adjusted to pH6.5 with calcium carbonate and filled semi-automatically in polypropylene bags for sterilization. The substrate thus prepared was found to be able to grow *Pleurotus eryngii* replacing rice or wheat straw. The appearance of the first flush fruitbodies took about 60 days from inoculation. Each bag, containing 1.2kg of the substrate with a water content of about 60% produced about 101g of fruitbodies in average if placed vertically without cutting any holes on the bags. Fruitbodies thus produced were mostly large with a thick context of pileus and a thick straight stipe. A bag with the same amount of substrate producted an average of 154g of fruitbodies if it was laid horizontally and a cross fissure about 2cm in length was cut at the bottom. Fruitbodies produced in this case were mostly small with a thin context of pileus and a thin bending stipe.

Key words : Cultivation, *Pleurotus eryngii,* Sawdust, Polypropylene bags.

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酸楊桃接菌式發酵之研究[1]

楊 淑 惠　王 惠 亮[2]

摘要：由傳統楊桃汁醃漬法中分離之菌種以酵母菌爲主，初步鑑定出 *Candida pelliculosa, C. inconspicua, C. ciferrii, Saccharomy ces cerevisiae* 等，在傳統醃漬過程中，會有少量醋酸產生，其可滴定酸度、草酸、抗壞血酸及胺基態氮等的含量經醃漬後會有較明顯的減少，以接菌式發酵製造之楊桃汁，因發酵時間短，未有醋酸被測得，而其他有機酸、pH 值、酸度、粗蛋白質及胺基態氮等的含量變化並不明顯。糖類在醃漬發在醃漬發酵初期即被大量消耗，到中，後期已無法測得。傳統醃漬楊桃汁的嗜好性品評得分1.0—4.0分不等，接菌式發酵楊桃汁的嗜好性品評得分3.0分。

關鍵詞：酸楊桃、發酵、菌株、接菌、成份。

楊桃汁具清涼退火、潤喉爽聲之功效（本草綱目，李時珍），長久以來在傳統飲料中即佔有一席之地，深受國人所喜愛，在本土食品再出發的研究上，頗受注目。楊桃品種很多，供鮮食之甜味種有二林種、秤錘種及馬來西亞種等，而製成飲用果汁則以酸味種爲主，全省栽植面積爲99.64公頃，包括本地種、五汴頭種等[9]。新鮮酸楊桃的可滴定酸度約爲0.68—1.1%，pH 值在1.37—2.01左右，糖度約在5.5—7.9Bx%左右；糖類主要爲果糖（fructose）、葡萄糖（glucose）和蔗糖（sucrose）；有機酸種類主要爲草酸（oxalic acid）、酒石酸（tataric acid）、蘋果酸（malic acid）、檸檬酸（citric acid）、琥珀酸（succinic acid）、反丁烯二酸（fumaric acid）及戊二酸（ketoglutaric acid）[2,6,9]等。酸楊桃的傳統醃漬法爲：加7~10%食鹽，以一層楊桃一層鹽的方式鹽漬，任其自然發酵（spontaneous fermentation），一般需醃漬約三個月。因每次自然發酵所產生之菌種不儘相同，使得每批次的風味、品質不一，且因滲出液的自然蒸散亦影響原汁收量。方、蔡氏[1,9]由酸楊桃發酵過程中分離、鑑定得知酵母菌菌株有 *Candida hellenicus, C. humicola, C. tropicalis, C. dattile, C. golbosa, C. krusei, C. magoliae, Cryptococcus neoformans* 及 *Hanseniaspora gerilliermondii* 等十種酵母菌株，蔡氏[9]以人爲嗅覺做爲香氣之官能評估，結果以 *C. humicola, C. pelliculosa, C. steatolytica, Kluyveromyces thermotloeran*及混合接種所呈現之香氣較佳。王[4]之研究，將酵母菌（Y—4）接種於新鮮楊桃汁，進行通氣及嫌氣發酵，僅需三至四天即可得發酵楊桃汁，風味頗佳。本試驗擬採控制發酵（controlled fermentation）方法，自行由傳統之自然發酵中分離優良菌株，經鑑定、馴化後，以接入純種（pure culture）或二種以上菌株方式進行酸楊桃純培養（pure culture）發酵，取代傳統之自然發酵，期能篩選出優良菌株，應用於實際生產，縮短發酵時間，維持產品之一定品質，並將此技術提供農戶及食品業者參考。

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材料與冰塊

一、試驗材料

以屏東縣鹽埔鄉九分熟以上之酸味楊桃（*Averrhoa caramola L*）果實爲試驗材料，分別採集八十四年夏季果及八十五年冬季果。

二、試驗方法

㈠楊桃汁製作方法：

1. 傳統發酵法：

酸味種楊桃經洗滌、瀝乾後稱重。將楊桃鋪平在圓桶內，灑上一層鹽。鹽總重爲楊桃總重的 7 %，如此一層楊桃一層鹽覆蓋竹網，並壓上重物，以便汁液滲出時，楊桃不致浮出液面感染雜菌，圓桶置於遮蔭通氣良好處，總計醃漬三個月，醃漬期間每二星期取樣分析一次。

2. 接菌發酵：

⑴菌種分離與鑑定

於不同時間取樣之楊桃原汁，塗佈於 PDA 上，逢機挑取10個單一酵母菌菌落移至 YM agar中，於25°C培養二天，進行酵母菌細胞型態特性分類做初步鑑定，酵母菌純化後，以 bioMerieux Vitek 公司生產之 api20C AUX，依其鑑定手續，於 YM aga 培養18至24小時內進行鑑定。再以 Biolog 生產之 YT MicroPlate 依其鑑程續，先以 BUY 培養18至 24小時內進行鑑定。

⑵菌液

取80ml 新鮮酸楊桃汁，加入 3 %鹽，經90°C加熱三分鐘，放冷後接入篩選出之優生菌株（共 4 株），於28～30°C以 100r.p.m. 振盪培養 24小時。

⑶試驗組

1.5升新鮮酸楊桃汁經加 3 %鹽、滅菌、冷卻後，接入已培養24小時之菌液（菌液濃度6 $\times 10^5$，接種量 5 %），於28—30°C，以100r.p.m. 振盪培養，經發酵五天後完成，發酵期間每日固定時間取樣分析。

㈡分析項目：

供試驗分析之楊桃汁，除了新鮮楊桃汁是從新鮮楊桃壓榨而得，其後之楊桃汁皆取自醃漬後自然滲出汁液或發酵液。

1. pH 值：以 pH meter 測定。
2. 可滴定酸度測定：取 5g 樣品加入10倍去離子水，以0.1N 氫氧化鈉滴定至 pH8.2。以草酸爲計算標準。
3. 有機酸分析[12]：楊桃滲出汁液，經離心後以0.45μm 濾過處理後，以日立高效液相層析儀測定，分離管 Aminex HPX-87H，管溫40°C，UV 偵測器210nm，流動相0.01N H_2SO_4，將結果與對照組比較，做有機酸鑑定，定量則與對照組面積比較換算。
4. 糖類分析[12]：樣品處理同上，以日立高效液相層析儀測定，分離管爲 Aminex HPX-87H，管溫43°C，RI 偵測器，流動相爲 0.01NH_2SO_4，鑑定及定量方法與有機酸相同。
5. 粗蛋白質測定[3]：取適量樣品於消化管中，加入催化劑及濃硫酸於氮分解爐中加熱分解，冷卻後蒸餾，以硼酸液收集蒸餾液，收集液以 0.1NH_2SO_4 滴定。每 ml0.1N 硫酸＝1.4006mg 之氮，以總氮量 ×6.25計算。
6. 胺基態氮測定：依中國國家標準 CNS 總號12630方法。

7. 生菌數之檢驗：依中國國家標準 CNS 總號10890方法，以 PCA 及YM ager 為培養基，於30°C培養2—3天後計算菌落數。
8. 糖度：取澄淸原液，以 ATAGO PR1 數字式糖度計測定。
9. 抗壞血酸測定：取適量樣品，加入偏磷酸溶液中，以2,6-Dichloropgenol indophenol-Na 滴定至粉紅色。
10. 菌種鑑定：以 bioMerieux Vitek 公司生產之 api20C AUX 及由 Bio log 生產之 YT MicroPlate 鑑定。
11. 風味品評：評定項目為色澤、香氣、味道及總接氣性，品評員為本分所分析室固定10人，品評樣品為發酵完成之酸味楊桃滲出液，經過濾、殺菌加入糖度 100 Brix之糖水，依一比四比例稀釋，以20°C之溫度供品評，經品評定所得之評分。

 1分：很差　2分：差　3分：尙可　4分：好　5分：很好

結果與討論

本次供試（屛東縣鹽埔鄉）之新鮮酸楊桃的可滴定酸度約為0.73%，pH 值在1.7左右，糖度為 6.3^0 Brix，糖類主要為果糖和葡萄糖，總糖含量約為4.83g%，有機酸種類主要為草酸，蘋果酸、琥珀酸及檸檬酸次之，總有機酸含量為0.91g%。酸楊桃醃漬低糖酸又添加食鹽的發酵環境，在此情況下微生物相的種類已被自然篩選，本試驗由傳統醃漬楊桃汁中所分離出的菌種主要為酵母菌，初步鑑定出 *Candida. pelliculosa, C. inconspicua, C. ciferrii, Saceharomyce s cerevisiae* 等四株菌，外型為圓型及長橢圓型，大小（2—3）×（2—5）μm，如圖1所示，其中 *S. cerevisiae* 為常見之酒精發酵菌，而以 *C. ciferrii* 菌株之活力最旺盛，經30°C48小時盪培養菌數可達10^8 CFU/ml，且該菌株為中、後段醃漬的優勢菌。四株菌單一接種、發酵的風味頗為相似，惟均較淸淡，為使楊桃接菌式發酵的風味更近以傳統醃漬楊桃的味道，本試驗採混合接菌法，將四株菌同時加入，於室溫中振盪發酵。

一、一般成份變化

蔬果經醃漬後成份常有消長，表1為酸楊桃以傳統醃漬法或接菌式發酵法發酵期間一般成份含量變化情形。酸楊桃以接菌式發酵法發酵，因發酵時間短，其發酵液之各項成份含量變化不明顯，酸度含量在0.68—0.72g%之間、pH 值在1.4—1.6左右、粗蛋白質含量約在0.14—0.17g%之間、胺基態氮含量則由 22.9mg/100g 微幅下降至 18.2mg/100g。以傳統醃漬法發酵者，其發酵液之 pH 值在2.0—1.8左右、粗蛋白質含量約在0.14—0.17g%之間，醃漬期間變化並不顯著，酸度則會由醃漬前的0.73g%漸漸下降至0.37g%，且前段下降幅度較中、後段明顯，此結果與前報相似[7]，胺基態氮含量會隨醃漬時間延長由22.89mg/100g 巨幅下降至8.98mg/100g。由於胺基態氮含量是 CNS 蔬果汁成份檢測上的檢驗項目，亦是食品廠收購發酵楊桃原汁的標準之一，故影響該成份之因素是品種、環境或微生物菌相等則有待深入探討。

二、糖類及有機酸含量變化

酸楊桃之糖類主要為果糖、葡萄糖和蔗糖[6,7,8]，本次供試驗之酸楊桃，為屛東縣鹽埔鄉地區性品種，其總糖含量約為4.83g%，以葡萄糖及果糖為主，蔗糖則無法測得，此現象可能與品種或成熟度有關，有等再進一步調查。糖類在醃漬發酵初期即被大量消耗，以傳統方式醃漬者，在第一、二週期間葡萄糖、果糖消耗率分別為80%、72%，第八週後已無法測得。接菌式發酵初期葡萄糖消耗率高達90%；果糖消耗率為62%，發酵至第四天葡萄糖已無法測得，果糖則仍有0.16g%的含量，如表2所示，傳統醃漬法或接菌式發酵法之糖類消耗情形頗為相似，葡萄糖被消耗的速率比果糖快，亦較先被耗盡，此結果與 Cancalon[10] 對柳橙汁所做試驗報告相似。若以碳源耗盡為發酵完成之指標，則傳統醃漬長達三個月的發酵似乎是可被縮短的，是否為風味熟成之考量有待探討。

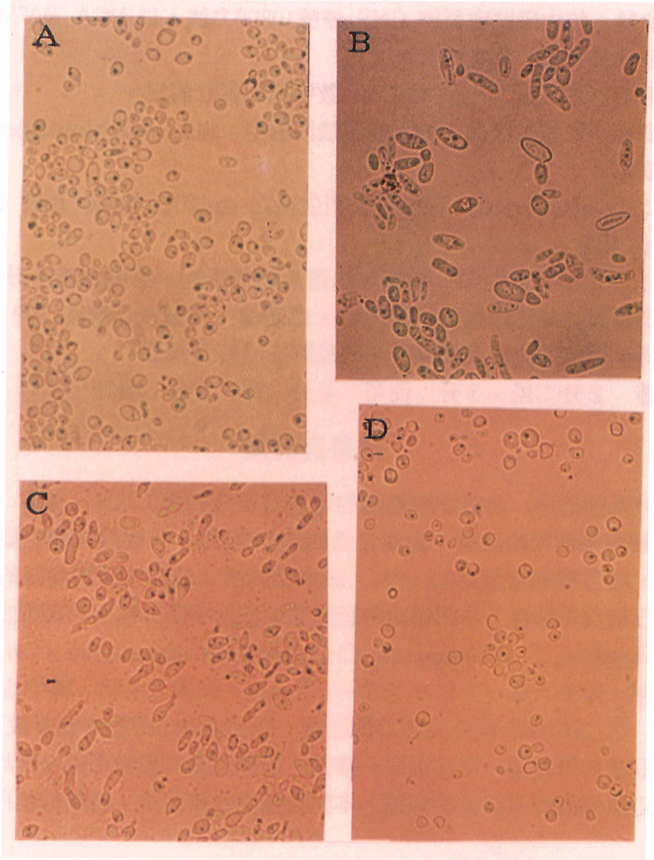


圖1. 由酸楊桃醃漬液分離出之酵母菌菌株

Fig. 1. Yeast strains observed under microscop x 400 from the exduate of tart carambola.
A：*Candida pelliculosa* B：*C. inconspicaua*
C：*C. ciferrii* D：*Saccharomyces cerevisiae*

表1. 酸楊桃經傳統醃漬法與接菌發酵法之一般成份含量變化

Table 1. Changes of composition of carambola fermentated by traditional and inoculating methods

Traditional method					Inoculating method				
Fermen tation (day)	Titratble acidity %	pH value	Crude protein g%	Amino nitrogen mg/100g	Fermen tation (day)	Titratble acidity %	pH value	Crude protein g%	Amino nitrogen mg/100g
0	0.73	1.7	0.16	22.9	0	0.72	1.6	0.16	22.9
14	0.37	2.0	0.15	16.1	1	0.69	1.5	0.17	20.2
28	0.39	2.0	0.15	15.8	2	0.70	1.5	0.16	20.8
42	0.37	1.8	0.16	13.6	3	0.68	1.4	0.16	21.0
56	0.38	1.9	0.15	12.9	4	0.70	1.4	0.15	20.1
70	0.36	1.7	0.15	11.4	5	0.70	1.4	0.14	18.2
84	0.36	1.8	0.14	8.9	—	—	—	—	—

酸楊桃的有機酸種類主要爲草酸、酒石酸、蘋果酸、檸檬酸、琥珀酸、反丁烯二酸及戊二酸[4,7,8,9]等，本次供試之酸楊桃其有機酸種類主要爲草酸、蘋果酸、琥珀酸。酸楊桃經傳統醃漬法發酵第二週後，會有醋酸產生，含量約0.08g%。大多數的有機酸會被微生物利用而減少[9]，以草酸、蘋果酸及抗壞血酸含量爲例，其草酸含量由0.72%下降至0.40g%左右，減少了44%，蘋果酸含量由

0.089%減少爲0.032g%，抗壞血酸含量明顯由12.3mg/100g減少爲6.5mg/100g。而接菌式發酵法發酵者，其草酸含量則下降至0.64g%，減少11%，蘋果酸含量及抗壞血酸含量則分維持在0.1g%至0.09g%及11～12mg/100g 之間，變化不明顯，如圖2、3。

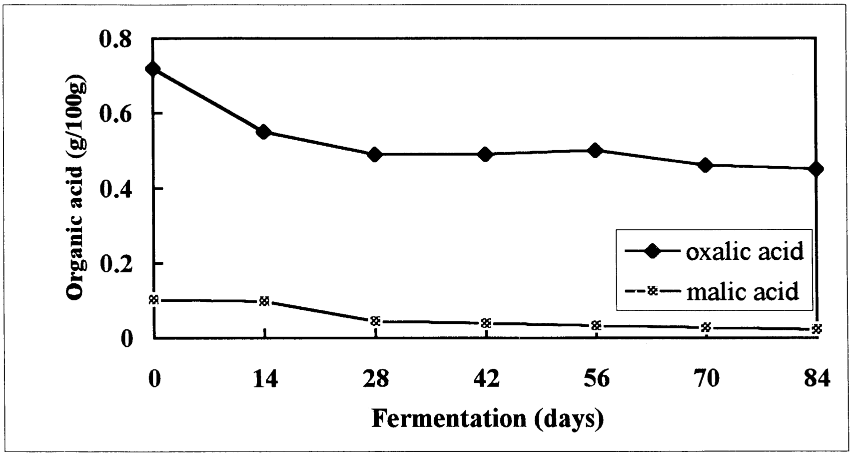
表2. 酸楊桃經傳統醃漬法與接菌發酵法之醣類含量變化

Table 2. Changes of sugar content of carambola fermentated by traditional and inoculating methods

Traditional method				Inoculating method			
Fermentation (day)	Glucose %	Fructose %	Sucrose %	Fermentation (day)	Glucose %	Fructose %	Sucrose %
0	1.581	3.251	ND[z]	0	1.581	3.252	ND
14	0.332	0.891	ND	1	0.158	1.250	ND
28	0.028	0.137	ND	0	0.067	0.488	ND
42	0.017	0.085	ND	0	0.030	0.269	ND
56	ND	ND	ND	4	ND	0.160	ND
70	ND	ND	ND	5	ND	ND	ND
84	ND	ND	ND	—	—	—	—

[z]ND：Not detected

(a)



(b)

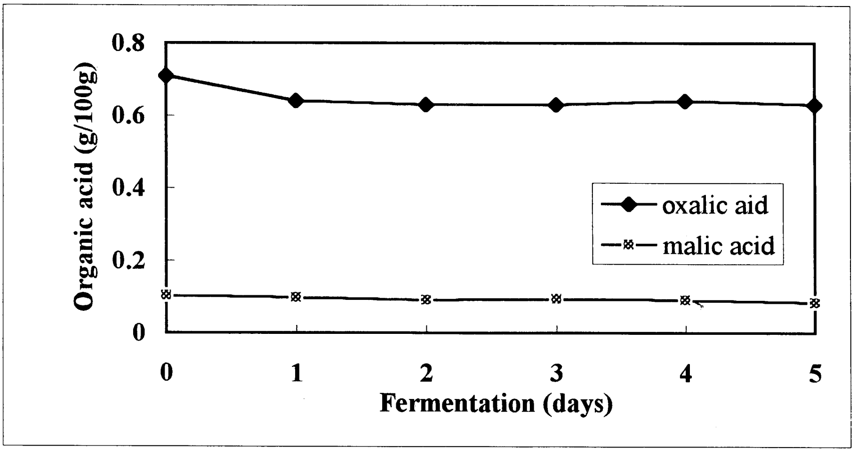
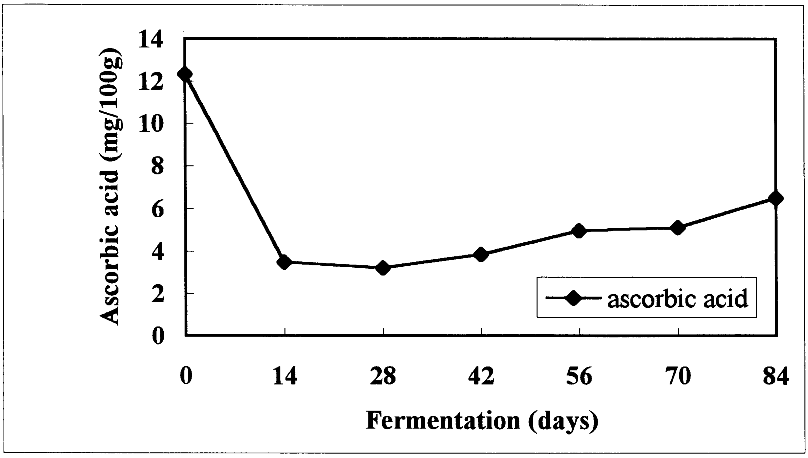


圖2. 酸楊桃於(a)傳統醃漬法與(b)接菌式發酵期間之有機酸變化

Fig. 2. Changed of organic acid of carambola fermentated by (a) traditioal pickled method and (b) inoculating method.

(a)



(b)

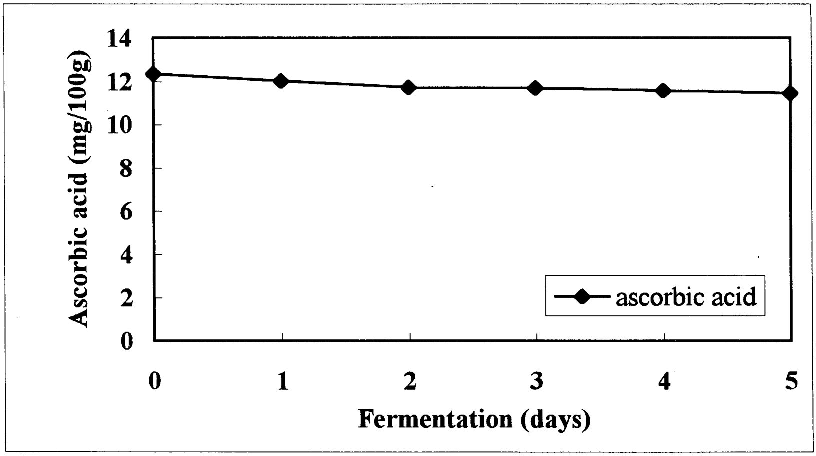


圖3. 酸楊桃於(a)傳統醃漬法與(b)接菌式發酵期間之抗壞血酸含量變化

Fig. 3. Changed of ascorbic acid contents of carambola fermentated by (a)traditioal pickled method and(b)inoculating method.

三、稀釋果汁品評

將收集之不同批次傳統醃漬楊桃果汁，及接菌式發酵楊桃果汁，以相同比例加糖水稀釋，由十名人員品評。品評結果如表 3 所示，接菌式發酵果汁的品評得分均在2.5～ 3 分左右，傳統醃漬果汁的品評得分則由 1 ～ 4 分不等。接菌式發酵果汁在口感上，澀味較傳統醃漬果汁重，風味上較清淡，且其香氣亦與傳統醃漬果汁不相同。傳統醃漬果汁風味濃郁，惟每批之色澤、香氣不同，亦有些批次因氣味不佳而品評得分較低者。故整體而言，接菌式發酵的品質尚稱良好，若在風味菌株選用、發酵時間再延長，以便增加草酸等酸類之消耗量等方面再做改進，製造出富於香氣、品質穩定的發酵楊桃汁是可以期待的。

依王氏[4]、蔡氏[9]之報告，以傳統方法或接菌方式發酵酸楊桃，都會有醋酸產生，含量最高可達0.23g%；前報[7]之傳統醃漬法亦有約0.1g%的醋酸產量，惟本次接菌方式發酵試驗並未測得有醋酸存在，推測可能是含量太低無法測得，或與菌株種類有關，依方氏、蔡氏[1,9]分離之酵母菌菌株有 *Candida hellenicus, C. humicola, C. tropicalis, C. dattile, C. golbosa, C. krusei, C. magoliae, Cryptococcus neoformans* 及 *Hanseniaspora gerilliermondii* 等十種酵母菌株，均與本次試驗所

分離出之菌株不盡相同，依 Pederson[11]之報告，溫度及鹽量會影響泡菜醃漬之菌相，是否爲菌相差異所致則有待再深入探討。

表3. 楊桃汁傳統醃漬法及接菌式發酵之官能品評

Table 3. The sensory evaluation of carambola juice fermentated by traditional and inoculating methods.

Method	Sensory evaluation										
	1	2	3	4	5	6	7	8	9	10	Total score
Traditional	2	4	3	2	1	2	2	1	2	3	22.0
Inoculating	3	3	3	3	2	3	3	2	3	3	27.0

n=5

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Studies on Tart Carambola Fermentation with Inoculating Method[1]

Shu-Hui Yang and Hui-Liang Wang[2]

Summary

Yeasts were the major microbes in carambola traditional pickled method. They are *Candida pelliculosa, C. inconspicua, C. ciferrii* and *Saccharomyces erevisiae.*
During the traditional pickled process, a small mounts of acetic acid was appeared. Titratable acidity, oxalic acid, ascorbic acid and amimo nitrogen contents decreased significantly after pickled by traditional method. However, fermentation by inoculating method acetic acid could not be detect and titratable acidity, oxalic acid and amimo nitrogen contents didn't change too much also. Most of sugars were rapidly metabolized by the micrboes during the early stage of fermentation, therefore, it is unabled to detect at middle and final stages. The sensory evaluation scores of traditional and inoculating methods were from 1.0 to 4.0, and 3.0, respectively.

Key words : Tart carambola, Fermentation, Strain, Inoculating, Copmposition.

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Effect of Releasing Trichogramma embryophagum (Hymenoptera:Trichogrammatidae) on Controlling Asiatic Corn Borer (Lepidoptera:Pyralidae) in Taiwan[1]

Bing-Huei Chen and Jih-Zu Yu[2]

Abstract: *Trichogramma embryophagum* Hartig, an exotic egg parasitoid, was evaluated in the corn fields at the experimental farm of Taiwan Agricultural Research Institute for its efficacy on parasitizing the eggs of the Asiatic corn borer, *Ostrinia furnacalis* Hubner in Taiwan. Results showed that *T. embryophagum* significantly increased the parasitism percentage of the *O. furnacalis* egg mass and the eggs within each mass up to 100% in the released plots comparing to that of the control in both spring and fall cropping seasons of 1993 and 1994. Also, *T. embryophagum* predominated over the indigenous *T. ostriniae and T. chilonis* in relative percentage recovered from the eggs of *O. furnacalis* collected in the released treatments. The plots with the release of *T. embryophagum* had significantly higher yield of fresh ear, less damage percentage, and higher weight and percentage of marketable ear than those of the control treatment in both cropping seasons of 1994. The percentage of marketable ear in released treatment was over 90% in both cropping seasons while that of the control was only 3.8% with 100% damaged fresh ear in the spring cropping season. Results from this study therefore revealed that the exotic egg parasitoid, *T. embryophagum* could be complementary to the indigenous *T. ostriniae and T. chilonis* in parasitizing the eggs of *O. furnacalis*. The biological control of the corn borer could be improved by the inoculative release of *T. embryophagum* in the fields.

Key words: Corn borer, *Trichogramma* egg parasitoids, Release, Biological control.

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INTRODUCTION

The Asiatic corn borer (ACB), *Ostrinia furnacalis* Hubner is the most serious insect pest of corn in Taiwan. It could damage leaves, tassels, silks, ears, and stalks of corn plants, and causes severe loss in yield. For its control, farmers used to applying insecticides and *Bacillus thuringiensis* when ACB larvae occurred at whorl and pollen heading stages. Because the consumers demand residue-free agricultural products, it would therefore be wise to adopt an alternative biological control method. Since mid-1980's, an indigenous egg parasitoid, *Trichogramma ostriniae,* has been released in the corn fields for controlling *O. furnacalis* in Taiwan [(6)]. Temperature has been reported affecting parasitization efficiency of several species of*Trichogramma*[(5,13)].This wasp could provide good parasitism on eggs of corn borer in fall cropping season, but the parasitism is unsatisfactory in spring cropping season especially when the weather is wet and the ambient temperature drops below 20°C[(3)]. Generally, ACB in Taiwan occurs more seriously in spring than in fall cropping season that releasing *T. ostriniae* alone is unable to obtain high enough parasitism to suppress the corn borer population below economic injury level.

Totally twenty exotic and indigenous *Trichogramma* species reared in the beneficial insect laboratory of Taiwan Agricultural Research Institute had been tested for their suitability to eggs of *O. furnacalis* in order to improve their parasitism on egg masses in spring cropping season. Results revealed that *T. embryophagum* and *T. evanescens* showed the most promising potential for parasitizing the corn borer eggs. Chen[(3)]reported that *T. embryophagum* had higher parasitism under 22°C, with longer longevity at 18°C, and predominated over *T. ostriniae* in recovery percentage from host eggs in laboratory conditions. Whether *T. embryophagum* performing in field conditions as well as that in laboratory is needed to be further tested.

Introduction of single or multiple species, or exotic or indigenous natural enemies for controlling a target insect pest is always a controversial issue among biological control workers[(7,10,11)]. The opposite opinion of having additive effect or competitive exclusion draws intensive argument. Researchers reported that simultaneously releasing two or more species of natural enemies may not be necessary permitting the occurrence of competitive interaciton because they might have different preferred microhabitats[(8)] or due to abundant host population[(11,14)]. Therefore, the objective of this study is to determine whether the release of the exotic *T. embryophagum* in corn fields may have adverse or complementary effect along with the indigenous *Trichogramma* species on the control of *O. furnacalis* in Taiwan.

MATERIALS AND METHODS

The plants: Super sweet corn, Honey 236, was planted at spacing of 90×30 cm in plots of total 0.6 ha in the experimental farms of Taiwan Agricultural Research Institute (TARI) at Wufeng, Taichung in both spring and fall cropping seasons of 1993 and 1994. The corn was grown on March 12 and August 25, 1993 for the spring and fall cropping season of 1993 respectively, while that of 1994 was on March 3, and August 26, 1994. The corn plants

received conventional fertilizer application and tillage management except no chemical application throughout the growing season. When the corn plants reached whorl stage, 20 plants from each of the four replicated plots of 0.05ha with 10 m apart were sampled, and the egg masses on each plant were collected and put individually into glass vial to check the parasitism rate and the recovery percentage of species before releasing *Trichogramma* egg parasitoids.

The parasitoids: Culture of the exotic *T. embryophagum* maintaining in the beneficial laboratory of TARI was used in this experiment. They have been reared and propagated in the laboratory for generations by parasitizing the eggs of rice moth, *Corcyra cephalonica* Stainton reared in the insectary. The emerged adult moths were collected daily and placed into oviposition cylinders for laying eggs. The deposited eggs were collected daily and sprayed on glued paper card of 50×30 cm in size. The eggs on the cards were then irradiated at 15 cm under UV light of 190 luxes for one hour to prevent the embryo from development before exposing to *Trichogramma* wasps for mass rearing.

Field release and sampling method: There were two treatments of with or without releasing *T. embryophagum* in this experiment. In spring and fall cropping seasons of 1993, field releases were made on May 10, 17, and 24, and on October 5, 12, 19, and 26 respectively. In spring and fall cropping seasons of 1994, field releases were conducted on April 20, 27, May 6, and 11, and on September 29, and on October 6, 13, and 20, respectively. Twenty egg cards each containing about 100 nearly emerging *T. embryophagum* pupae were randomly stapled underneath the leaves of corn plants in the releasing plots. The other field of 0.2 ha consisting of four plots of 0.05 ha each and about 200 m apart from the released site was used as the control where only the indigenous *T. ostriniae* and *T. chilonis* were present. One week before the first releasing till the end of each respective cropping season, 20 plants were randomly sampled weekly from each plot and the egg masses of corn borer on each plant were thoroughly collected. Only two samplings were made on May 17 and 24 for the spring cropping season in 1993 due to continuously raining for 3 weeks that destroyed the corn plants in the plots. The collected egg masses was each put into a glass vial sealed with parafilm and kept in chamber at 25°C. The parasitized eggs then turned dark whereas those unparasitized began to hatch, and their respective number was recorded to determine the percentage of parasitism for egg masses and for individual egg. The parasitized egg mass in each vial was allowed to let the parasitoids emerge and die. Specimen in each vial were sexed, and those males were mounted and identified by using Olympus BHS microscope to count the frequency of each species. At harvest, 20 plants were randomly sampled and the ears on each plants were collected and weighted. Number of ear with or without damage was counted and weighted. Harvested ears will be categorized into unmarketable and marketable ones included those without or with only slight damage by ACB. The percentage of egg mass parasitized, the percentage of eggs parasitized per mass, the recovery percentage of each *Trichogramma* species from each sample, the weight of fresh ears, the percentage of ear damaged, and the weight and the percentage of marketable ears were tabled and compared between the released and the control plots by PROC ANOVA in Statistical Analysis System

and t-Test was used to separate means at different levels of significance.

RESULTS AND DISCUSSION

In spring cropping season of 1993, percentage of egg mass parasitized by the indigenous *T. ostriniae* and *T. chilonis* was 73.8% in the released fields, then reached 96.7% and up to 98.6% within two weeks after releasing the exotic *T. embryophagum* which contributed about 25% increment in parasitism and was significantly higher than that of the control at each of respective sampling date (Table 1). Only three samplings were made in this season due to continuously raining for two weeks that destroyed the corn plants in fields.

Table 1. Parasitism percentage of egg mass of *O. furnacalis* and progeny sex ratio in the treated and the control plots before and after releasing *T. embryophagum* in the spring cropping season of 1993

Date[z] M/D	% parasitism of egg mass (Mean±SE)[y]		% parasitism of eggs (Mean±SE)		Progeny sex ratio	
Treated	Control	Treated	Control	Treated	Control	
5/10	73.8±3.8	5.0± 5.0	55.8±4.9	5.5± 5.5	1.6	4
5/17	96.7±1.9**	10.0±10.0	92.8±2.5**	10.0±10.0	1.9	22
5/24	98.6±2.5*	70.0± 9.8	91.3±2.3*	67.3± 9.6	1.4	3.8

[z] Planting date on March 12, 1993.
[y] * : $p<0.05$; ** : $p<0.01$, t test.

Before the field release of *T. embryophagum* on October 5 in fall cropping season of 1993, the indigenous *Trichogramma* species contributed only 16.7% and 0% of parasitism rate on the egg masses of *O. furnacalis* in the released and in the control plot respectively. One week after releasing the exotic species into corn fields, the percentage of parasitism sharply increased to 93.3%, and was 100% at the end of season while that of the control at each of respective sampling date was significantly lower ranging from 0 to 22.2%(Table 2). Similar results were obtained in the percentage of *O. furnacalis* egg mass parasitized in both spring and fall cropping seasons in 1994(Tables 3 & 4). Before releasing *T. embryophagum,* none of egg masses sampled on April 20, and on September 29, 1994 was parasitized. One week after release, the parasitism rates were 76.9% and 83.6% in the released plots which were significantly higher than that in the control for the spring and the fall cropping season respectively. The parasitism rate in the released plots increased with the plants grew toward maturity and was up to 100% at the end of both seasons in 1994(Table 3 & 4). The results showed that *T. embryophagum* and *T. ostriniae* did not interfere with each other in parasitization efficiency, and were successful in sharing the hosts which is similar to the relationship between *T. brassicae* and *T. cacoeciae* exploiting the eggs of flour moth, *Ephestia kuehniella,* reported by Bouletreau *et al.*[1].

Table 2. Parasitism percentage of egg mass of *O. furnacalis* and progeny sex ratio in the treated and the control plots before and after releasing *T. embryophagum* in the fall cropping season of 1993

Date[z] M/D	% parasitism of egg mass (Mean±SE)[y]		% parasitism of eggs (Mean±SE)		Progeny sex ratio	
	Treated	Control	Treated	Control	Treated	Control
10/ 5	16.7±16.7	0	16.7±16.7	0	2.7	—
10/12	93.3±6.3**	22.2±14.5	87.8± 7.0**	9.2±6.6	1.4	—
10/19	87.5±4.2**	8.3± 8.3	75.4± 7.6**	2.3±2.3	1.7	—
10/26	76.9±2.5**	20.0±20.0	70.1±11.9**	4.2±4.2	1.8	—
10/ 2	100**	0	92.9±3.1**	0	1.5	—

[z] Planting date on August, 25, 1993.
[y] * : $p<0.05$; ** : $p<0.01$, t test.

Table 3. Parasitism percentage of egg mass of *O. furnacalis* and progeny sex ratio in the treated and the control plots before and after releasing *T. embryophagum* in the spring cropping season of 1994

Date[z] M/D	% parasitism of egg mass (Mean±SE)[y]		% parasitism of eggs (Mean±SE)		Progeny sex ratio	
	Treated	Control	Treated	Control	Treated	Control
4/20	0	0	0	0	—	—
4/27	76.9±6.8**	0	70.3±6.6**	0	1.8	—
5/ 6	89.4±3.6**	8.6±4.8	84.0±3.8**	6.6±3.8	1.5	2.1
5/11	92.6±4.2**	27.5±6.6	89.6±2.9**	26.3±6.8	1.2	1.3
5/18	98.7±2.3**	24.6±8.5	95.3±3.1**	23.2±7.1	1.4	1.4
5/25	100**	69.2±7.5	98.2±2.1**	67.4±7.3	1.7	1.4
6/ 1	100**	0	88.6**	0	1.2	—

[z] Planting date on March 3, 1994.
[y] ** : $p<0.01$, t test.

Table 4. Parasitism percentage of egg mass of *O. furnacalis* and progeny sex ratio in the treated and the control plots before and after releasing *T. embryophagum* in the fall cropping season of 1994

Date[z] M/D	% parasitism of egg mass (Mean±SE)[y]		% parasitism of eggs (Mean±SE)		Progeny sex ratio	
	Treated	Control	Treated	Control	Treated	Control
9/29	0	0	0	0	—	—
10/ 6	83.6±7.1**	0	79.8±8.5**	0	2.1	—
10/13	84.5±6.6**	35.0±11.9	83.2±1.0**	27.6±10.3	1.5	2.1
10/20	92.1±2.0**	33.5± 1.5	98.2±1.9**	30.9± 2.5	1.5	1.6
10/27	100**	36.5±12.9	100**	33.3±11.5	2.4	1.5
11/ 3	97.2±2.8^{ns}	90.5± 5.0	95.2±2.8^{ns}	84.1± 7.9	1.8	1.5
11/10	100^{ns}	83.0± 7.1	93.5±6.5^{ns}	80.9± 8.8	1.4	1.4

[z] Planting date on August 26, 1994.
[y] ** : $p<0.01$, t test.

The percentage of eggs parasitized per egg mass was calculated. Results from both spring and fall cropping seasons in 1993 showed that the parasitism rate in the released plots increased respectively from 55.8% and 16.7% to 92.8%and 87.8% at one week after releasing the exotic egg parasitoids while that of the control especially in the fall cropping season was very low ranging from 0% to as high as 9.2% only (Table 1 & 2). Percentage of individual egg parasitized per egg mass in the released plots was significantly higher than that of the control at each sampling date in the spring and most of except the last two samplings in the fall cropping season in 1994(Table 3 & 4). The higher parasitism percentage of eggs within egg mass was, the fewer larvae of O. *furnacalis* could hatch and consequently, the lesser damage on corn plants. Results from this study showed that the exotic *T. embryophagum* has a complementary effect on the indigenous *T. ostriniae* and *T. chilonis,* and is capable of enhancing the parasitism rate to the *O. furnacalis* egg masses.

More female progenies emerged than those of male in the released plots with sex ratio ranging from 1.2 : 1 to 2.4 : 1 after field release. In the spring cropping season 1993, more females emerged from the control check than males with ratio up to 22:1. This sex ratio should be unfavorable to *T. ostriniae* populations in the fields because few males will result in producing all male progenies by the unmated female wasps since the parthenogenensis of *T. ostriniae* is arrhenotokous while *T. chilonis* has been found with thelytokous type of reproduction in Taiwan[(4)].

The percentages of different *Trichogramma* species recovered from each sample collected in both cropping seasons in 1993 and 1994 were listed in Tables 5−8. Before field release, only the indigenous *T. ostriniae* and *T. chilonis* recovered from the fields in spring and fall cropping season in 1993, but none of them was found in both seasons in 1994. After releasing, *T. embryophagum* predominated over the other egg parasitoids each sampling in both cropping seasons in 1993 and 1994. Results from egg masses of *O. furnacalis* collected on May 17, 1993 showed that *T. embryophagum* occupied 73.3% of the emerged wasps with 23.6% of *T. ostriniae,* and 3.1% of *T. chilonis*. In fall cropping season 1993, *T. embryophagum* constituted 77.0%, 77.4%, 77.4%, and 89.1% of recovery rate which was significantly higher than that of the two domestic species collected on October 12, 19, 26, and November 2, respectively. Similar results were obtained in spring and fall cropping seasons of 1994, *T. embryophagum* reached the highest 93.5% of recovery rate with 5.6% of *T. ostriniae,* and 0.9% of *T. chilonis* on October 6, 1994. Only *T. ostriniae* and *T. chilonis* recovered from the control in both cropping seasons and years. Results coincided with those from the laboratory and the greenhouse studies that *T. embryophagum* predominated over *T. ostriniae* in parasitizing host eggs when they were simultaneously released for exploiting the eggs of corn borer [(3)]. Also, species displacement did not happen in this study which proved that *T. embryophagum* has the ability to discriminate between parasitized and unparasitized ACB eggs. Similar result was reported by Klomp *et al.*[(12)] on *T. embryophagum* that could discriminate parasitized and unparasitized eggs of the flour moth.

Table 5. Relative percentage of *Trichogramma* species recovered from egg masses of *O. furnacalis* collected before and after releasing *T. embryophagum* in the spring cropping season of 1993

Species	Sampling date (month/day)							
	5/10		5/17		5/24		5/31	
	Treated	Control	Treated	Control	Treated	Control	Treated	Control
T. ostriniae	96.7a[z]	100a	23.6b	100a	37.3b	77.8a	—	—
T. chilonis	3.3b	0b	3.1c	0b	2.4c	22.2b	—	—
T. embryophagum	0b	0b	73.3a	0b	60.3a	0c	—	—

[z] Means in each column followed by the same letter are not different significantly at 5% level according to Duncan's New Multiple Range Test.

Table 6. Relative percentage of *Trichogramma* species recovered from egg masses of *O. furnacalis* collected before and after releasing *T. embryophagum* in the fall cropping season of 1993

Species	Sampling date (month/day)									
	10/5		10/12		10/19		10/26		11/2	
	Treated	Control	Treated	Control	Treated	Control	Treated	Control	Treated	Control
T. ostriniae	71.4a[z]	0	19.5b	0	17.0bc	0	20.5b	0	10.8bc	0
T. chilonis	28.6b	0	3.5c	0	5.6c	0	2.1c	100	0c	0
T. embryophagum	0c	0	77.0a	0	77.4a	0	77.4a	0	89.1a	0

[z] Means in each column followed by the same letter are not different significantly at 5% level according to Duncan's New Multiple Range Test.

Table 7. Relative percentage of *Trichogramma* species recovered from egg masses of *O. furnacalis* collected before and after releasing *T. embryophagum* in the spring cropping season of 1994

Species	Sampling date (month/day)													
	4/20		4/27		5/6		5/11		5/19		5/25		6/1	
	T[z]	CK	T	CK	T	CK	T	CK	T	CK	T	CK	T	CK
T. ostriniae	0	0	21.2b[y]	0	23.2b	55.6a	16.9bc	73.8a	14.0bc	70.6a	13.6bc	69.1a	20.5b	0
T. chilonis	0	0	5.3c	0	4.0c	44.4a	3.1c	26.2b	2.5c	29.4b	3.9c	30.9b	5.5c	0
T. embryophagum	0	0	73.5a	0	72.8a	0b	80.0a	0c	83.5a	0c	82.6a	0c	74.0a	0

[z] T : Treated ; CK : Control.
[y] Means in each column followed by the same letter are not different significantly at 5% level according to Duncan's New Multiple Range Test.

Table 8. Relative percentage of *Trichogramma* species recovered from egg masses of *O. furnacalis* collected before and after releasing *T. embryophagum* in the fall cropping season of 1994

Species	Sampling date (month/day)											
	9/29		10/6		10/13		10/20		10/27		115/3	
	T[z]	CK	T	CK	T	CK	T	CK	T	CK	T	CK
T. ostriniae	0	0	5.6bcy	0	7.7bc	70.3a	6.3bc	83.9a	7.8bc	76.4a	8.3bc	78.8a
T. chilonis	0	0	0.9c	0	1.8c	29.7b	2.3c	16.1b	0.8c	23.6b	3.6c	21.2b
T. embryophagum	0	0	93.5a	0	90.5a	0c	91.4a	0c	91.4a	0c	88.1a	0c

[z] T : Treated ; CK : Control.
[y] Means in each column followed by the same letter are not different significantly at 5% level according to Duncan's New Multiple Range Test.

Effect of releasing *T. embryophagum* on the yield of corn was significant between treatments in both spring and fall cropping seasons in 1994(Table 9). In spring 1994, the weight of fresh ears per 20 plants, the percentage of ears damaged, the weight and the percentage of the marketable ears was 5.8 kg, 41.1%, 5.3 kg, and 90.7% respectively for the release plots while that of the control was 1.5 kg, 100%, 1.0 kg, and 3.8%, respectively with significant difference between treatments. In fall 1994, the respective item recorded for the releasing plots was 6.7 kg, 17.8%, 6.3 kg, and 94.0% which was significantly better than that of the control of 3.8 kg, 68.9%, 1.4 kg, and 36.8%, respectively. The results showed that releasing *T. embryophagum* into corn fields reduced the damage of corn ears and increased its marketable ear yields.

Table 9. Difference in yield, damage, and marketable percentage of fresh ears between plots with or without releasing *T. embryophagum* in the spring and the fall cropping season of 1994

Treatment	Weight (kg) of fresh ears/20 plants		% fresh ears damaged		Weight (kg) of marketable ears/20 plants		% marketable ears	
	Spring[z]	Fall	Spring	Fall	Spring	Fall	Spring	Fall
Release	5.8**	6.7*	41.1	17.8	5.3**	6.3**	90.7**	94.0*
Control	1.5	3.8	100*	68.7*	0.1	1.4	3.8	36.8

[z] $*p<0.05$; $**p<0.01$, t Test.

Trichogramma species have been widely used for the control of major insect pests [2,6,15]. Recently, the impact of exotic wasps on non-target hosts has been concerned by researchers [9]. Based on the data obtained from this study, the problem that concerned is unlikely to happen for *T. embryophagum.* Since the release of this exotic species in 1993, it has shown additive effect along with the local *Trichogramma* species against *O. furnacalis.* However, its field occurrence suggested that it has not yet established in Taiwan because it did not recover from each sample collected before release in both spring and fall cropping seasons in 1994. Nevertheless, survery on this exotic species should be continued and closely checked to make sure its establishment in Taiwan. Results from this study revealed that *T. embryophagum* can be supplementary to *T. ostriniae* in checking *O. furnacalis* at acceptable low level especially in spring cropping season when the corn borer is much abundant and the environmental conditions are unfavorable to the activities of the local parasitoid. The relationship between *T. embryophagum* and *T. ostriniae* truly illustrated what stated by Moon[14] as "following the introduction of species B, coexistence with species A may be a common event, even when A and B compete for several resources, and that the competitive exclusion may not adequately apply to the heterogeneous real world".

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釋放外來卵寄生蜂*Trichogramma embryophagum* Hartig 防治亞洲玉米螟[1]

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摘要：在臺灣省農業試驗所之試驗農場進行田間釋放，評估外來卵寄生蜂*Trichogramma embryophagum* Hartig 對亞洲玉米螟*Ostrinia furnacalis* Hubner 卵之寄生效果。在1993年與1994年春秋兩季之試驗結果顯示，此種外來卵寄生蜂在釋放區可增加對玉米螟卵塊與卵粒之寄生率，最高可達100%而與對照無釋放區呈顯著之差異。定期自釋放區與對照區取樣玉米螟卵塊，比較各蜂種回收比率之結果顯示，在釋放區 *T. embryophagum* 均比另外兩種本地卵蜂 *T. ostriniae* 與 *T. chilonis* 爲優勢。釋放與否對玉米穗收量之影響，結果顯示 *T. embryophagum* 卵寄生蜂在1994年春秋兩季於釋放區可顯著增加玉米鮮穗重、減少穗受害率、增加可上市穗率與穗重，而與對照區呈顯著之差異。在釋放區之玉米穗可上市穗率，無論春秋兩季均可達90%以上。而對照區之玉米穗受害率高達100%而可上市穗率僅有3.8%。綜合本試驗結果顯示，*T. embryophagum* 卵寄生蜂與另外兩種本地種 *T. ostriniae* 與 *T. chilonis* 對玉米螟卵之寄生俱互補作用，定期釋放該寄生蜂將可加強玉米螟之生物防治。

關鍵詞：玉米螟、玉米螟赤眼卵寄生蜂、釋放、生物防治。

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木瓜葉蟎生物防治之研究[1]

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摘要：木瓜之葉蟎種類經調查主要爲神澤氏葉蟎（*Tetranychus kanzawai* Kishida））， 其次是柑桔葉蟎（*Panonychus citri* (McGregor)）及皮爾斯葉蟎（*T. piercei* McGregor ），而赤葉蟎（*T. cinnabarinus* Boisduval）發生較少，故防治對象是以神澤氏葉蟎爲主。南部木瓜園中，葉蟎族群自12月開始建立，在２～４月達最高峰，５月後因梅雨季節，密度驟減。田間釋放智利捕植蟎（*Phytoseiulus persimilis* Athias-Henriot）及法拉斯捕植蟎（*Amblyseius fallacis* (Garman)）皆可有效防治木瓜葉蟎，而智利捕植蟎之效果較好，每次釋放約500隻／株之捕植蟎，釋放約２至３次即可有效防治葉蟎，釋放位置以下位葉最好。1988～1989年在臺中霧峰之露地栽培木瓜園，釋放法拉斯捕植蟎二次，釋放天敵區有葉蟎6.1隻／葉，對照區有178.6隻／葉；1992年在高雄縣美濃鄉之網室栽培木瓜園，釋放法拉斯捕植蟎二次，至掀網時，釋放天敵區有葉蟎14.3隻／葉，噴藥區有169.8隻／葉，而對照區則有599.8隻／葉；1993年在屏東縣高樹鄉之網室栽培木瓜園，釋放法拉斯捕植蟎三次，至掀網時，釋放天敵區已沒有葉蟎，噴藥區有41.4隻／葉，而對照區則有469.0隻／葉。

關鍵詞：木瓜、葉蟎、捕植蟎、生物防治。

木瓜（*Carica papaya* L.）爲本省重要熱帶果樹之一，目前之栽培面積約3,000公頃，其主要栽培地區集中於本省中南部及東部地區，主要之病蟲害有輪點病、白粉病、葉蟎、蚜蟲及介殼蟲等[1,6,8,9,10]。近年來應用交叉保護技術及栽培耐病品種[2,19]，對輪點病之防治已有明顯效果；1986年起復利用網室栽培方式，阻隔媒介蚜蟲傳播木瓜輪點病之防治效果更高達97%[3]。網室栽培所種植之木瓜品種爲不抗病但品質較佳之臺農二號木瓜，栽培面積估計已達1,000公頃。此法雖能有效防止病毒病之發生，但對葉蟎則無阻絕效果，相反地，此種栽培方式給予葉蟎更佳生態環境，葉蟎不但提前發生，且爲害之程度亦較露地栽培者更爲嚴重。木瓜對葉蟎之爲害極爲敏感，往往先自下位葉掌狀葉基部沿放射葉脈兩側爲害，被害葉表初呈灰白色瘤狀突起，逐漸因水份及養液傳導受阻，被害嚴重處枯死破孔，終至全葉黃化而脫落。有報告提出神澤氏葉蟎（*Tetranychus kanzawai* Kishida）對殺蟎劑已產生抗性[18]，而農民爲求防治蟎類，往往長期過量施藥，同時木瓜對殺蟎劑甚爲敏感，，而導致嚴重藥害發生，使農民損失甚鉅。在國外，智利捕植蟎（*Phytoseiulus persimilis* Athias-Henriot）及法拉斯捕植蟎（*Amblyseius fallacis* (Garman)）均被利用來防治葉蟎，且成效卓著[14,17]。在本省並先後自國外引進此二種捕植蟎，在草莓、桑及茶上獲致顯著的成效[4,5,7,13]。本研究之目的在於利用此二種捕植蟎試驗對露地木瓜園和網室木瓜園防治神澤氏葉蟎之效果，作爲進一步防治推廣之依據。

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材料與方法

一、木瓜葉蟎發生消長之種類調查

神澤氏葉蟎周年消長調查主要在鳳山分所進行，以露地及網罩栽培木瓜各一區，區內各種植木瓜60株，自1990年12月至1991年7月共調查八個月，每隔14天調查一次，每次逢機取10株，每株採掌狀葉1葉，攜回室內以鏡檢調查蟎數（包括幼、若蟎及成蟎）。另於高屏地區選擇二園木瓜園，定期每月採集一次，每次各採10葉，調查木瓜葉蟎之發生種類。

二、神澤氏葉蟎在木瓜上之發育情形

在臺中霧峰進行神澤氏葉蟎在木瓜上不同溫度時之發育情形，分別在30、25、20及15°C之生長箱內（相對濕度60～80%），以培養皿（直徑6公分）墊以消毒棉，並浸以蒸餾水，然後剪一直徑約5公分的木瓜葉下表朝上置於上，每葉接上1隻神澤氏葉蟎雌蟎飼育，每處理10隻，如木瓜葉黃化，即予更換，以觀察其在木瓜葉上之發育情形。

三、捕植蟎在木瓜上之移動觀察

1990年在鳳山進行，在網室栽培之木瓜園內，取約具20葉大小的木瓜植株，將智利捕植蟎與法拉斯捕植蟎100隻（各齡期合計），分別釋放於木瓜植株之下層（第1葉片）、中部（第10葉片）或頂部（第20葉片）等三種不同處理，每處理重複二株，共十二株，於釋放後6、12及24小時觀察二種捕植蟎於木瓜植株不同部位釋放後之移動情形。

四、田間生物防治試驗

以農業試驗所研發之大量繁殖技術[15,16]飼養捕植蟎，其方法如下：在網室內用水稻育苗盤培育大豆苗，每盤豆苗約700～800株，育苗約7～20天，載至溫室內，每盤接入約50,000隻二點葉蟎，約4～7天，再接入捕植蟎約3,000隻，經10～14天，每盤可繁殖得20,000隻捕植蟎。

㈠露地栽培木瓜葉蟎生物防治試驗：

於臺中縣霧峰鄉之露地栽培木瓜園內做初步試驗，設2小區，每小區各50株，分別爲釋放法拉斯捕植蟎及未釋放之對照區。自1988年8月9日開始調查，當日並於採樣後第一次釋放捕植蟎，每株約1,000隻，釋放後二星期調查一次，每次逢機取樣20株，每株取掌狀葉1葉，攜回實驗室內鏡檢調查，計算葉上之神澤氏葉蟎及法拉斯捕植蟎之蟎數。於10月18日調查時發現植株之葉蟎密度有升高的趨勢，於是第二次釋放法拉斯捕植蟎，釋放前與釋放後每二星期調查一次，至隔年2月21日止，共調查16次。

㈡網室栽培木瓜葉蟎生物防治試驗：

鳳山分所於1991年開始大量繁殖捕植蟎，提供高屏地區約網室木瓜試驗大量釋放之用。

1. 大寮試驗區：

於1991年在高雄縣大寮鄉網室栽培木瓜園進行，設8處理，分別爲釋放法拉斯捕植蟎及智利捕植蟎每株各500、1,000、1,500隻、藥劑防治區及不釋放對照區，每處理5株，重複3次，按逢機區集排列。自1991年1月13日開始調查，於1月31日及3月27日分別釋放一次，共二次，每株以500、1,000及1,500隻密度釋放，釋放點以木瓜植株的第一朵花爲基準；藥劑防治區於1月15日、2月10日、3月10日及4月10日噴藥四次，所噴施的藥劑爲50%芬佈賜可濕性粉劑3,000倍及42%克芬蟎水懸劑3,000倍輪流使用，當時木瓜上尙無推薦藥劑，此藥劑是農民經常使用之藥劑。釋放前與釋放後每二星期調查一次共調查9次，調查時每株採掌狀葉1葉，攜回實驗室內鏡檢調查並記錄神澤氏葉蟎之蟎數（包括幼、若蟎及成蟎）。

2. 美濃試驗區：

於1992年在高雄縣美濃鄉網室栽培木瓜園進行，設３處理，分別爲釋放法拉斯捕植蟎、藥劑防治區及不釋放對照區。生物防治區設５重複，每重複200株；藥劑防治區200株；對照區20株。自1992年３月20日開始調查，並於３月20日及４月18日分別釋放法拉斯捕植蟎，共二次，每株釋放500隻，釋放於木瓜植株的第一朵花處；並同時於藥劑防治區噴藥，先施藥劑爲42%克芬蟎水懸劑4,000倍，後施50%芬佈賜可濕性粉劑3,000倍。釋放前與釋放後每二星期調查一次，至掀網共調查５次，每區逢機調查10株，每株採掌狀葉１葉，攜回實驗室內鏡檢調查，並記錄神澤氏葉蟎之蟎數（包括幼、若蟎及成蟎）。

3. 高樹試驗區：

於1993年在屏東縣高樹鄉網室栽培木瓜園實行，設３處理，分別爲釋放法拉斯捕植蟎、藥劑防治區及不釋放對照區。生物防治區設５重複，每重複200株；藥劑防治區500株；對照區20株。自1993年３月23日開始調查，並於３月23日、４月20日及５月18日分別釋放捕植蟎，共三次，每株500隻，釋放於木瓜植株的第一朵花爲基準，並同時藥劑防治區噴藥，藥劑爲42%克芬蟎水懸粉4,000倍及50%芬佈賜可濕性粉劑3,000倍輪流施用。釋放前與釋放後每二星期調查一次，至掀網共調查６次，每區逢機調查10株，每株採掌狀葉１葉，攜回實驗室內鏡檢調，並記錄神澤氏葉蟎之蟎數（包括幼、若蟎及成蟎）。

結果與討論

一、木瓜葉蟎發生消長及種類調查

1981年溫和李曾報告爲害木瓜之蟎類以赤葉蟎（*Tetranychus cinnabarinus* Boisduval）爲主，但經田間調查結果，木瓜上之葉蟎種類主要爲神澤氏葉蟎（*T. kanzawai*），其次是柑桔葉蟎（*Panonychus citri* (McGregor)）及皮爾斯葉蟎（*T. piercei* McGregor），赤葉蟎發生較少，且調查發現造成木瓜葉嚴重枯死破孔者爲神澤氏葉蟎，而柑桔葉蟎並不會對木瓜葉造成爲害，所以防治對象是以神澤葉蟎爲主。

在露地及網室栽培之木瓜葉蟎發生消長情形列於圖１，木瓜於1990年11月31日定植，於12月７日開始調查，由圖１上可看出網室內葉蟎之密度在３月雨量少時，已達每葉10,151.8隻葉蟎，超出露地每葉7,538.5隻葉蟎很多，４月中旬因高雄地區有下冰雹，使得露地之葉蟎密度驟降，６月進入梅雨期，網室內葉蟎密度降低至每葉只有7.5隻葉蟎，露地則有122.5隻葉蟎葉，至７月雨量稍減，葉蟎密度又有升高之趨勢。７月底時因大雨將露地栽培之木瓜浸死，且網室亦受風害，將網室吹破，以致於８月後之資料無法調查。由以上的調查發現，葉蟎在南部高屏地區低溫及低濕的環境下，密度會急速增加，而至高溫多雨的環境時，密度則驟降。木瓜的栽培期是一整年的，但冬季是其栽培初期，若不在早期防治好葉蟎之爲害，木瓜則無法正常開花結果，影響品質極大。

二、神澤氏葉蟎在木瓜上之發育情形

神澤氏葉蟎在不同溫度下，以木瓜苗飼育結果列於表１，分別在30、25、20、15°C之生長箱內（相對濕度60～80%），由卵到成蟎其發育速度分別爲7.8、11.6、20.8及40.1日，其發育速度幾與神澤氏葉蟎在茶上之情況相同[11]，分別爲7.1日、10.4日、18.4日及41.4日。其每升高 5°C，發育速度即增倍。產卵量在20及25°C均達90個以上，而在茶上30°C時產卵量只有76個。在南部地區冬季氣溫幾乎維持在20～25°C左右，且木瓜栽培期自每年的８～10月至隔年的５～８月開始採收，栽培初期正適合神澤葉蟎在木瓜上之繁殖。

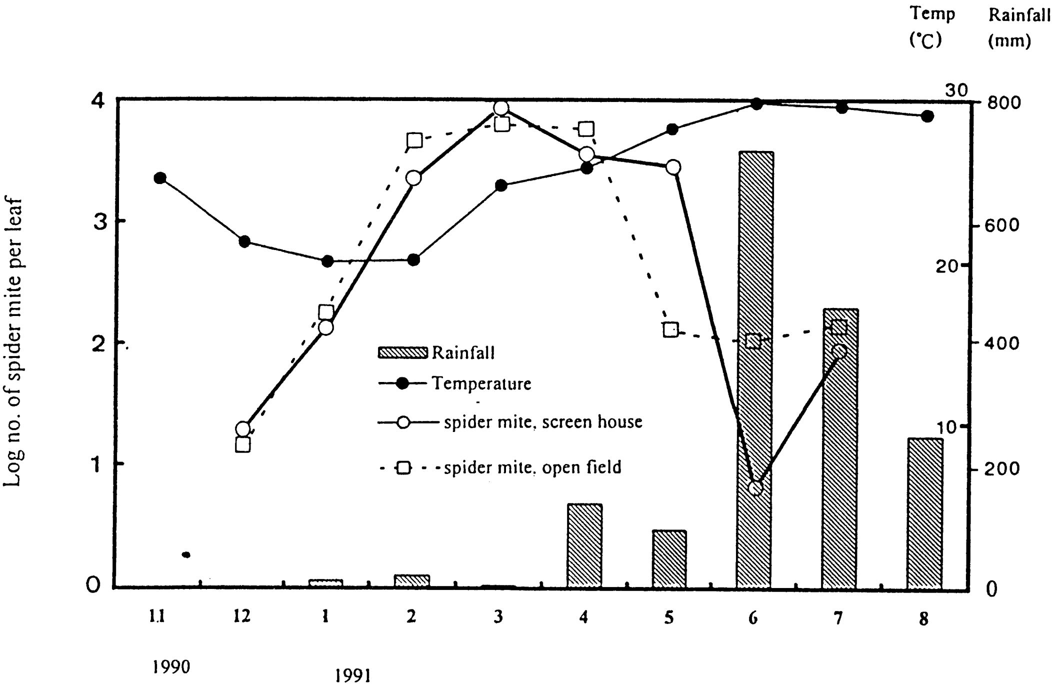

圖 1. 露地與網室栽培木瓜葉蟎周年消長調查

Fig. 1. Seasonal occurrence of the spider mite on papaya in open and screened fields.

表 1. 不同溫度下神澤氏葉蟎在木瓜上發育期長、產卵量及成蟎壽命

Table 1. Duration (days) of immature stages, fecundity and adult longevity of *Tetranychus kanzawai* on papaya under different temperatures.

Stage	Duration at Temperature°C			
	15	20	25	30
Egg	16.0	7.2	4.2	3.1
Larva	6.8	4.1	1.8	1.1
Nymphochrysalis	3.1	1.8	1.1	0.7
Protonymph	4.6	1.9	1.3	0.8
Deutochrysalis	2.9	1.7	1.1	0.6
Deutonymph	5.1	2.4	1.1	0.7
Teleiochrysalis	3.3	2.0	1.2	0.8
Total	40.1	20.8	11.6	7.8
Eggs/♀	60.4	94.9	90.2	—
Longevity	40.1	27.0	20.2	—

三、捕植蟎釋放在木瓜上之移動觀察

一般葉蟎在植物上爲害，當葉蟎密度增高，植物營養條件不利於葉蟎生育時，葉蟎多有向上爬行至植物頂稍和葉稍，並吐絲結網的行爲(12)，在木瓜上也有此情形。爲求防治效果，欲觀察捕植蟎在木瓜植株上是否亦有向上爬行之習性，另智利捕植蟎與法拉斯捕植蟎之移動性，與釋放之部位密切相關，故分別釋放於下層、中部及頂部三處，釋放後 6 、12及24小時觀察其移動情形，結果列於表 2 ，結果可看出智利捕植蟎在12小時時已開始移動，而法拉斯捕植蟎則在原地不動；於24小時後，在下層的捕植蟎已移動至第 7 ～ 8 葉，而釋放於中部的捕植蟎則移動至15～17葉，由此可知釋放於下層及中部之捕植蟎皆有向上之趨勢。由表 2 資料來看，釋放24小時後，智利捕植蟎在頂部者移動 4 葉，在中部者移動 9 葉，在下層者移動13葉；而法拉斯捕植蟎在頂部者移動 4 葉，在中部及下層者均移動 7 葉，明顯可見智利捕植蟎活動力較強，且二種捕植蟎均具向上移動之習性，釋放於木瓜中部及頂部之捕植蟎，僅停留在第 9 片葉以上之葉片上，而下層葉蟎密度高度之葉片，無法有效防治，故藉此調查之結果，決定將捕植蟎之釋放點定位在木瓜下層葉之葉柄基部，以有效防治葉蟎。

表 2. 智利捕植蟎及法拉斯捕植蟎在木瓜上釋放後移動情形

Table 2. Leaf positions where *P. persimilis* and *A. fallacis* were found after release on papaya.

Leaf position of release[z]	PP[y]			AF[y]		
	6hrs	12hrs	24hrs	6hrs	12hrs	24hrs
1	1	1,2,8	1～3,5,6,8,13	1	1	1～4,7
10	10	9～10,16	9～13,15～17	10	10	10～15,17
20	20	19,20	17～20	20	20	17～20

[z]Number of leaf position was counted from the bottom in a plant.
[y]PP : *P. persimilis* AF : *A. fallacis*.

四、田間生物防治試驗

(一)露地栽培木瓜葉蟎生物防治試驗：

1988年 8 月至1989年 2 月於臺中縣霧峰鄉進行，結果列於圖 2 。8 月 9 日當葉蟎密度達1,141.5隻／葉時，第一次釋放天敵，3 日後發生大風雨，導致葉蟎密度大幅下降，所幸捕植蟎已立足，故在天敵釋放區之葉蟎下降速度較對照區爲快，而捕植蟎密度下降，不足以壓制葉蟎時，導致第二波葉蟎族群之上升，但在天敵釋放區葉蟎上升速度較對照區爲緩慢，葉蟎豐度亦較對照區爲低。10月18日做第二次天敵釋放，葉蟎族群迅速降低維持至次年 2 月21日均不再大發生；而對照區此時葉蟎族群密度仍上升到每葉5,054.4隻，隨後在捕植蟎上升至每葉10.8隻後旋即迅速下降，結果與天敵釋放區相似。依此次試驗結果可發現捕植蟎可移動至很遠的範圍，可是因爲本試區爲露地栽培之故，捕植蟎與葉蟎皆可藉風力遷移至遠處，但若在網室內可能就無法藉由風力來遷移了；並可證明法拉斯捕植蟎確可於木瓜露地栽培情形下防治木瓜葉蟎。

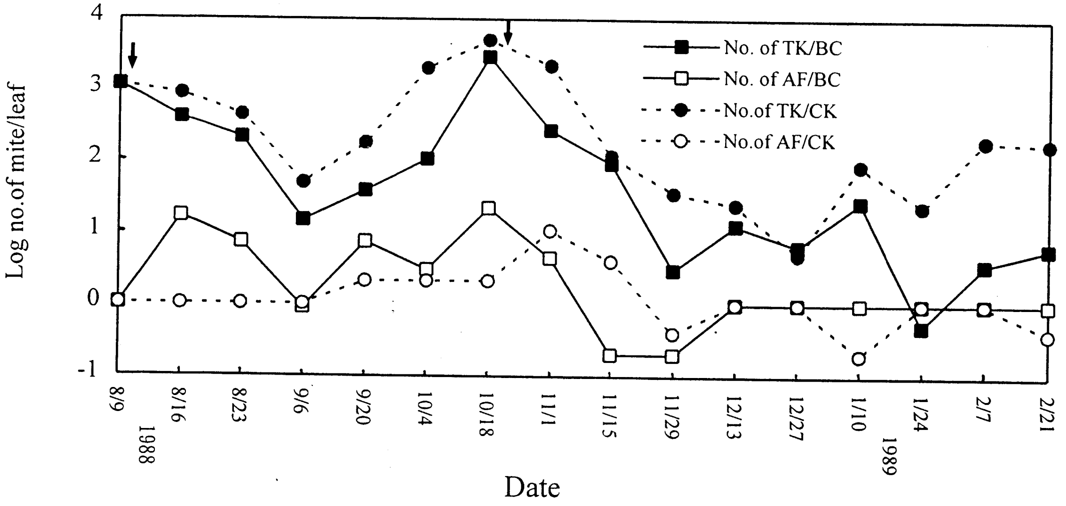

圖 2. 臺中露地木瓜試區釋放法拉斯捕植蟎防治神澤氏葉蟎之效果

Fig. 2. Effectiveness of biological control of *T. kanzawai* by *A. fallacis* on papaya in open field at Taichung. ↓: release of predator. AF: *A. fallacis*. TK: *T. kanzawai* BC: biological control.

㈡網室栽培木瓜葉蟎生物防治試驗：

1. 大寮試驗區：

在1991年 1 月高雄縣大寮鄉所作之釋放密度試驗：結果顯示兩種天敵三種不同釋放量（500隻／株、1,000隻／株、1,500隻／株），效果均甚顯著（如圖 3 及圖 4），因本實驗主要是測試在何種密度下就有效防治葉蟎，因此分繪兩圖。兩種天敵之三種釋放密度與藥劑防治處理效果差不多，因農民施藥採固定時間施藥，所以葉蟎密度一直維持在低密度之下，而三種釋放量的處理因天敵繁殖來不及釋放，所以至 1 月31日才第一次釋放天敵，釋放後二星期，天敵釋放區之葉蟎密度旋即降低，當葉蟎於捕植蟎釋放後約二個月，密度才又升高，於是在 3 月27日做第二次釋放，二星期後密度又降低，至 4 月25日掀網時葉蟎密度一直都維持在低密度。而對照區則一直維持在每葉200～300隻葉蟎，在 1 月27日因大雨葉蟎密度稍降，至 3 月27日時因對照區葉蟎爲害嚴重以致於葉片掉落，只剩心葉可調查，因此圖中之葉蟎密度驟降，但至 4 月25日時密度又再上升至每葉1,831.4隻葉蟎。試驗結果兩種捕植蟎三處理間，智利捕植蟎之抑制能力由圖 3 及圖 4 可看出第二次釋放後抑制葉蟎密度之能力較持久，二重天敵釋放量在500隻／株時，應可有效防治木瓜葉蟎。

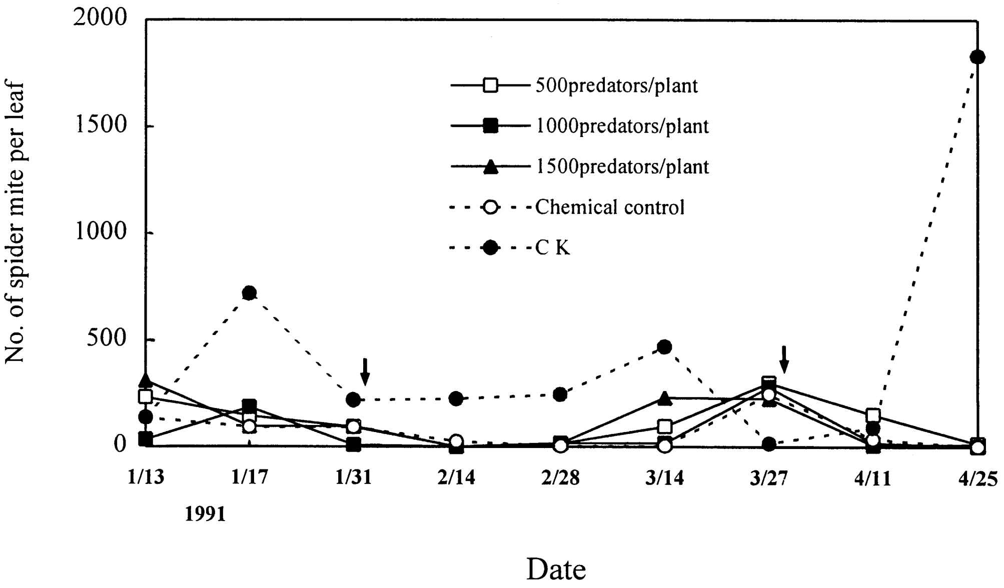

圖 3. 大寮試區釋放不同密度之智利捕植蟎和化學防治對防治神澤氏葉蟎之比較

Fig. 3. Comparison on the effectiveness of *P. persimilis* released in different numbers and chemical applications for controlling *T. kanzawai* on papaya at Ta Liao. ↓ : release of predator.

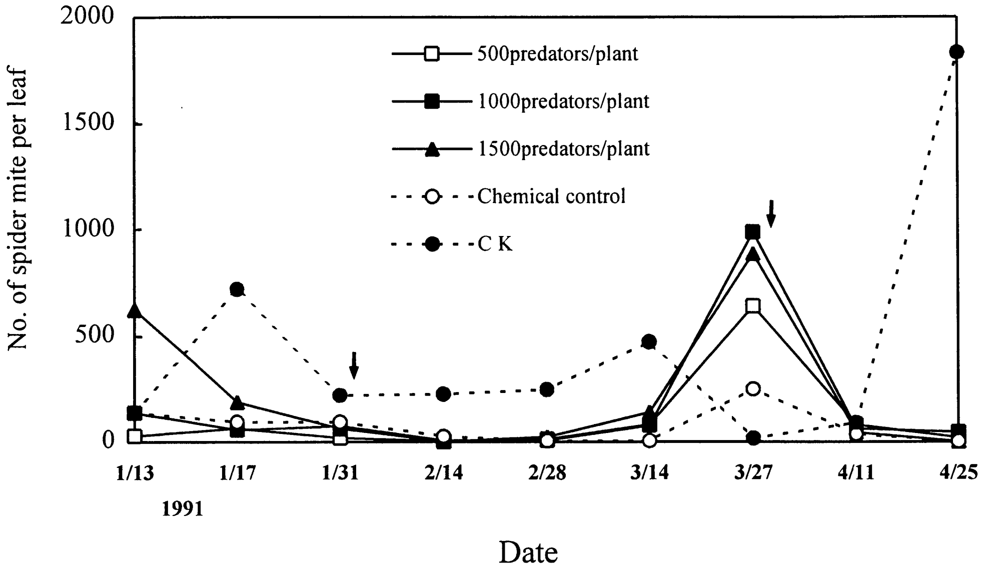

圖 4. 大寮試區釋放不同密度之法拉斯捕植蟎和化學防治對防治神澤氏葉蟎之比較

Fig. 4. Comparison on the effectiveness of *A. fallacis* released in different numbers and chemical applications for controlling *T. kanzawai* on papaya at Ta Liao. ↓ : release of predator.

2. 美濃試驗區：

雖然大寮試驗中，智利捕植蟎之防治效果優於法拉斯捕植蟎，但試驗時所用之捕植蟎來源是由本所應用動物系在臺中霧峰所繁殖的種源，爲減少運輸往返，自1991年開始將大量繁殖捕植蟎之技術轉移至鳳山分所進行，當時發現智利捕植蟎在繁殖過程中，會較不易繁殖，可能是因爲南部氣候熱的關係，而法拉斯捕植蟎則較能適應，故於高屏地區較適宜法拉斯捕植蟎之大量繁殖，所以在以下二次的試驗皆採用法拉斯捕植蟎來釋放。

於1992年在高雄縣美濃地區之試驗，採固定釋放量及釋放時間，因木瓜葉對葉蟎之爲害極爲敏感，每次當葉蟎密度升高時才釋放捕植蟎，再經 1～2 星期的捕食時間，木瓜葉已被爲害得枯死破孔，因此本次試驗決定採與農民定期噴藥時間一致釋放，固定釋放量採每株釋放500隻法拉斯捕植蟎，定期釋放則採間隔一個月，於 3 月20日及 4 月18日各釋放一次捕植蟎，其結果如圖 5 ，釋放時同時噴藥，之後葉蟎密度皆有下降的趨勢，至 5 月15日時，對照區密度持續增加至599.8隻葉蟎／葉，噴藥區則有169.8隻葉蟎／葉，而釋放天敵區只有14.3隻葉蟎／葉。釋放天敵區與藥劑防治區雖都可有效防治葉蟎，但釋放天敵之效果較藥劑防治爲佳，本次試驗採與農民施藥間隔時期同步釋放捕植蟎，發現可有效壓制葉蟎之再發生，因此可定期一個月釋放一次，以達防治之效果。

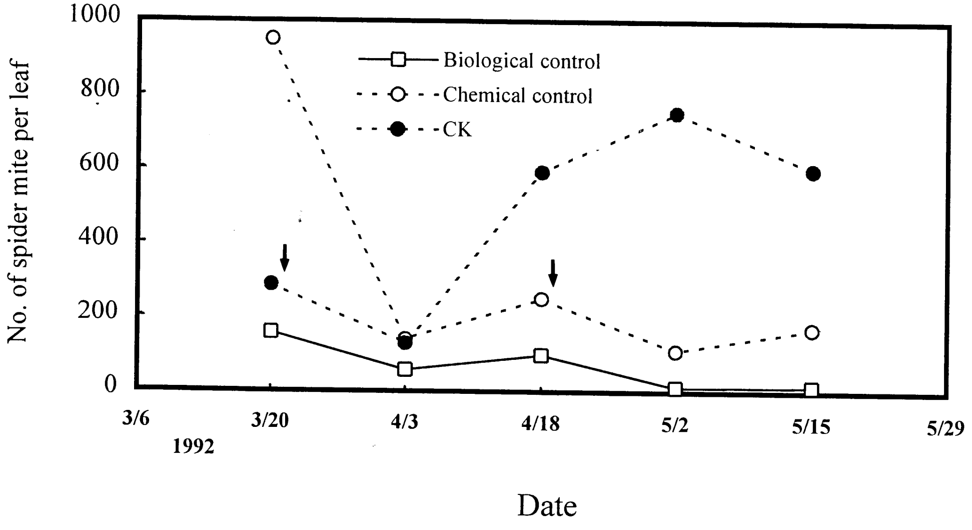

圖 5. 美濃試區釋放法拉斯捕植蟎防治木瓜園神澤氏葉蟎之試驗

Fig. 5. Biological control of *T. kanzawai* on papaya by releasing *A. fallacis* at Mei Nung.
↓ :release of predator.

3. 高樹試驗區：

於1992年在屏東縣高樹地區試驗釋放法拉斯捕植蟎時，再得到與美濃試驗相類似之效果，釋放後密度即有下降（圖 6 ）。因採固定釋放時間一個月，於 3 月23日、 4 月20日及 5 月18日共三次釋放，至 6 月 1 日調查時，對照區之葉蟎已增加至469隻／葉，噴藥區也有41.4隻／葉，而釋放捕植蟎區已沒有葉蟎爲害了。由此可知只要適期釋放天敵，定可有效防治葉蟎。

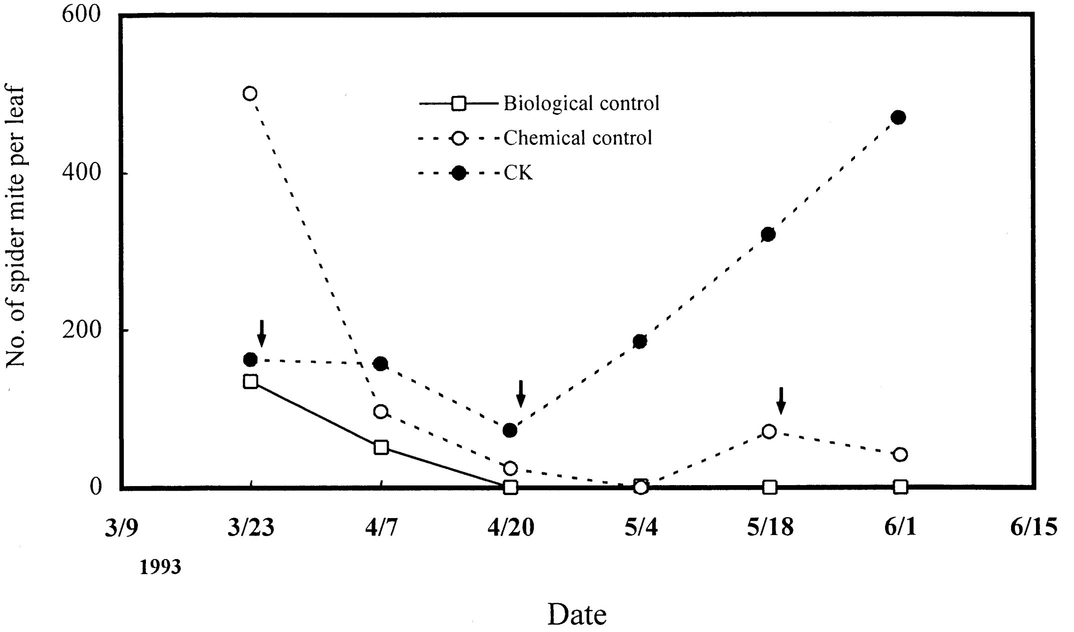

圖 6. 高樹試區釋放法拉斯捕植蟎防治木瓜園神澤氏葉蟎之試驗

Fig. 6. Biological control of *T. kanzawai* on papaya by releasing *A. fallacis* at Kao Shu.
↓:release of predator.

綜合以上之結果，可確認智利捕植蟎與法拉斯捕植蟎對木瓜上之神澤氏葉蟎皆具有防治效果，且智利捕植蟎之防治能力較法拉斯捕植蟎爲優。木瓜生長栽培時期長，每年 8 ～10月種植，至隔年 5 ～ 8 月採收，網室皆於颱風季節前， 6 ～ 7 月時掀網。當時農民無法相信不用噴農藥即可防治葉蟎，接受生物防治意願低，致使試區都很難尋得，往往木瓜都已結小果時才尋得試區，所以捕植蟎大都只釋放 2 ～ 3 次，至掀網即停止釋放，故資料不多，但已可看出捕植蟎之防治潛力無窮。

因木瓜栽培區幾乎多集中於高屏地區，且都以網室栽培，而南部地區氣候不適宜智利捕植蟎之繁殖，故以採用法拉斯捕植蟎來防治木瓜上之神澤葉蟎爲宜，其效果亦極爲優良。

木瓜近幾年已漸成國人生活中必需水果之一，其經濟價值也隨之提高了。爲了防止感染木瓜輪點病的機會，因而採網室栽培以得到高品質之木瓜，但網室中葉蟎是其最嚴重的問題，且又有抗藥性之產生。本計畫即在利用生物防治來解決農民的問題，但在推廣上由於捕植蟎之生產往往不能及時供應農民之需要，因此捕植蟎商品化生產應是迫切需要解決的問題。如能成功的利用捕植蟎來防治木瓜葉蟎，使農民不因葉蟎爲害而蒙受損失，進而減少農藥之施用，將爲農民和消費者之福音。

誌　　謝

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Studies on Biological Control of Spider Mites on Papaya[1]

Hsiu-Hwa Hao[2], Hui-Liang Wang[2], Wen-Tai Lee[3] and Kang-Chen Lo[3]

Summary

The kanzawa spider mite, *Tetranychus kanzawai* Kishida is the most common spider mite problem on papaya, followed by *Panonychus citri* (McGregor) and *T. piercei* McGregor, and *T. cinnabarinus* Boisduval occurs only sporadically. Seasonal occurrence of the spider mite on papaya occurs mainly from February to April. The population decreased after May due to the rainfall. Bothe phytoseiid predators, *Phytoseiulus persimilis* Athias-Henriot and *Amblyseius fallacis* (Garman), gave effective control on *T. kanzawai*. *P. persimilis* was more effective than *A. fallacis* when each time 500 predators/plant were released in total of two or three times in the test field. The best releasing position on plnat was found in the lower leaves. By releasing *A. fallacis* twice, the result showed that only 6.1 kanzawa spider mites/leaf could be found in the biological control plot, whereas 178.6 mites/leaf in the untreated plot in open papaya field in Wufeng, Taichung during 1988—89. By releasing *A. fallacis* twice under screenhouse condition, only 14.3 mites/leaf could be found in the biological control plot, compared to 169.8 mites/leaf in chemical control plot and 599.8 mites/leaf in the untreated plot on papaya in Mei Nung test field in Kaohsiung in 1992. Similar test was conducted in Kao Shu test field in Pintung in 1993. The result showed that spider mite could not be found in the biological control plot. However, 41.4 mites and 469.0 mites/leaf were found in chemical contro plot and untreated plot. respectively.

Key Words : Papaya, Spider mite, Phytoseiid, Biological control.

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瓜果實蠅誘殺劑不穩定性研究

—乃力松及克蠅之分解作用[1]

鄭　允[2]　古德業[3]　高靜華[2]　黃毓斌[2]

摘要：東方果實蠅誘殺劑，含毒甲基丁香油，在1992—93年成品發生褐變，以致藥效消退。經研究發現，主要原因來自誘殺劑中之乃力松受光分解，脫溴成爲二氯松後，再分解爲無效成份，經試以茶色瓶遮光，即可大幅提昇誘殺劑之穩定性；誘殺劑中之甲基丁香油則無明顯分解情形。瓜實蠅誘殺劑中之乃力松亦有類似的受光分解問題，而另一主成份克蠅則有自發性的水解現象，似與常態下室溫及光線之變化無關。克蠅經解離乙酸根後形成 p-phenyl-2-butanone，而失去誘集瓜實蠅之作用。

關鍵詞：東方果實蠅、瓜實蠅、誘殺劑、光分解。

本省採用滅雄技術防治東方果實蠅（*Bactrocera dorsalis* Hendel），所用誘殺劑之配方係以甲基丁香油與乃力松混合(1)。1994年以前本省北部以該誘殺劑浸泡之纖維板懸掛於田間，而中南部則以瓶裝之誘殺劑倒置於誘殺器內，以藥液緩慢釋入置於下方之小片纖維板上，分別進行誘殺。但由於1992～93年間，瓶裝誘殺劑發生嚴重變質，藥液色澤變黑，對東方果實蠅雖尙有誘集力，但致死率消退，以致農民拒絕使用該批藥劑，1993年之防治工作亦因而停頓。1994年 3 月農林廳特指定臺灣省農業試驗所研究誘殺劑變質之原因，並實施品質之管制與改進。此外，因瓜實蠅（*Bactrocera cucurbitae* Coquillett）之誘殺劑亦由甲基丁香油、克蠅及乃力松混合配製，也有相同之褐變情形，故一併進行其品質穩定性之研究。經探討後發現，常用之金屬容器並非造成誘殺劑變質之原因，但測試中發現光線，尤其是日光，似乎是最易造成誘殺劑褐變之主要原因，因此特就兩種誘殺劑受光後各主要成份之分解情形進行測試。瓜果實蠅誘殺劑主要成份受光分解導致藥效消退之研究，最早於1994年11～12月間即完成室內室外之比較觀察，並經初步測試及確立分析方法。爲解析各成份間之相互作用及分解速率，1995～96年再於相同之試驗狀況下進行連續取樣、成份比較及定量分析，故本論文內之試驗乃係經多次初試後，所再進行之系列性分析。

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材料與方法

一、試驗材料

甲基丁香油(Methyl eugenol，98%)，西德 Bayer 公司出品；乃力松原體(Naled，95%)，由青山化工公司提供；克蠅(Cuelure，98%)，購自美國 ICG 公司；二氯松乳劑(DDVP，50% EC)係榮民化工廠出品。透明及茶色玻璃瓶(容量20ml)、纖維板、甲醇。分析儀器爲氣相層析儀(Shimadzu GC14A-FID)及質譜儀(Shimadzu GC-MS QP 2000A)。

二、試驗方法

(一)供試藥劑之處理：誘殺劑分別以茶色及透明玻璃瓶各盛裝5ml，置於室內及室外進行觀察，共分四組處理：(1)透明瓶／室外(2)透明瓶／室內(3)茶色瓶／室外及(4)茶色瓶／室內。處理(3)及(4)分別爲室內及室外兩種環境下，非光照因子之對照組。所測試兩種誘殺劑爲：

1. 果實蠅誘殺劑：依植物保護手册登記之配方[1]，混合甲基丁香油及乃力松。
2. 瓜實蠅誘殺劑：依植物保護手册登記之配方[1]，混合甲基丁香油、克蠅及乃力松。

(二)取樣：本研究試驗期間爲1996年4月至7月，取樣時間爲配製試劑之當天（第0天）及其後的第2天、6天、14天、27天、41天及58天，共計7次，每樣品取0.1ml 後以2.5ml 甲醇稀釋，進行下列之儀器分析。

(三)分析方法：

1. 以1μl樣品稀釋液注入 GC-FID 分析，依(1)滯留時間及(2)峰形面積之積分爲計算依據。分析之毛細管分析柱規格爲25QC5/BP1 5.0，在180°C常溫下進行分析。乃力松滯留時間（R.T.）爲6.3分鐘（圖1a），二氯松之 R.T. 爲1.4分鐘（圖2a），克蠅之 R.T. 爲5.8分鐘（圖8a)，甲基丁香油之 R.T 則爲2.5分鐘（圖4a）。
2. GC-MS 分析所用之樣品與 GC-FID 相同，但毛細管分析柱規格爲25QC2／BPl 1.0，溫度程式之設定爲始溫170°C，4分鐘後開始升溫，每分鐘上升7°C，溫度昇至240°C後，維持20分鐘。乃力松標準品之 R.T. 爲11.0分鐘（圖1b），二氯松標準品之 R.T. 爲4.1分鐘（圖2b)，克蠅之 R.T. 爲10.5分鐘（圖11a)，甲基丁香油之 R.T. 爲6.4分鐘（圖6a、11a)。

結　果

供試誘殺劑分別置於室內及室外，進行觀察及樣品成份解析。其中，室內處理之透明玻璃瓶內誘殺劑有逐漸褐化的現象，但程度甚爲輕微；置於茶色瓶中之誘殺劑則無褐化現象。而置於室外之處理，透明瓶中誘殺劑有嚴重褐化現象，茶色瓶裝之誘殺劑則無褐化情形。第58天時取各處理傾入小透明玻璃瓶中，目測比較即可區分其褐變程度之差異，並照相存證如圖3及7。上述置於室內外之樣品在兩個月中連續取樣，其各主成份之分解情形如圖4、5、8、9及10。

一、果實蠅誘殺劑（甲基丁香油＋乃力松）

以 GC-FID 分析時，第0天樣品中之甲基丁香油及乃力松之 R.T. 分別爲2.5及6.4分鐘(圖4a)，而第58天樣品中之乃力松含量大幅降低（圖4b，R.T.＝6.4分鐘），且出現原配方中未有的物質，其 R.T. 爲1.4分鐘。再以 GC-MS 鑑定，乃力松（Scan No. 253）之 R.T. 爲11分鐘（圖6a），其質譜見圖6c；而誘殺劑中出現之分解物（Scan No.45）之 R.T. 爲4.1分鐘（圖6a)，其圖譜見圖

6b，經比對與二氯松相符（圖 2b）。該兩處之析出物均具有質量爲109及79之明顯特徵，不同之處爲前者有質量爲145之特徵，與乃力松完全相同，而後者之 R.T. 及質譜有質量爲185之特徵，與二氯松標準品完全相符。而第58天樣品中，乃力松與二氯松峰形面積合計爲原配方中乃力松之53%（乃力松佔35%，二氯松佔18%，圖 4b），其餘47%已完全分解而無法檢出，此外，另一主成份甲基丁香油則無顯著的分解現象。

置於室外之處理，以透明玻璃瓶包裝的誘殺劑中之乃力松分解程度最高，達46.9%，而置於室內者僅有少量分解，約2.4%（圖 5a）。不論置於室內或室外者，茶色瓶內誘殺劑所含之乃力松，均僅有1.7%分解（圖 5b）。

二、瓜實蠅誘殺劑（甲基丁香油＋克蠅＋乃力松）

由室內、外觀察的結果顯示，室內透明瓶內誘殺劑雖有逐漸褐化的現象，但程度輕微；置於茶色瓶中之誘殺劑則無褐化現象。置於室外者，透明瓶中之誘殺劑褐化現象嚴重，而茶色瓶中之誘殺劑則無褐化情形（圖 7）。其變化大致與果實蠅誘殺劑相同，但相同處理之褐化程度更爲迅速且嚴重。

以 GC-FID 分析比較第 0 天及第58天之樣品時（圖 8），甲基丁香油均無明顯分解現象。乃力松的分解物中，亦有 R.T. 爲1.4分鐘之二氯松成份出現，與果實蠅誘殺劑中的情形相類似，但更爲迅速及嚴重。置於室外透明瓶中之誘殺劑，其乃力松分解達60.5%，置於室內者則僅分解5.3%（圖 9 a），而茶色瓶包裝者不論置於室內或室外，乃力松之分解僅介於6.5%～9.4%之間（圖9b），雖遠低於室外透明瓶之處理，但已較同樣處理之果實蠅誘殺劑爲高，顯然混合三種物質對乃力松之分解有更促進之作用。

置於室內及室外透明瓶之瓜實蠅誘殺劑所含之克蠅，分解程度分別爲13.4%與23.2%（圖10a）；但置於茶色瓶處理之克蠅在室內分解17.4%，室外則僅有12.1%分解（圖10b），各處理間之差異小於試驗誤差而呈不顯著的結果，顯見克蠅的分解與此試驗室內室外處理之不同溫度及光線條件，無明顯相關，而可能爲一種自發性的水解作用(autolysis)。

瓜實蠅誘殺劑中之乃力松及其分解物在 GC-FID 及 GC-MS 之滯留時間及圖譜，均與果實蠅誘殺劑中所測得者完全相同，亦有二氯松之中間物存在（圖 8b，R.T.＝1.4分鐘；圖11a，R.T.＝4.1分鐘）。而質譜分析時（圖11a），克蠅分解物之 Scan No. 爲186（圖11b），其滯留時間 R.T. 爲8.8分鐘，與克蠅（Scan No.237，R.T.＝10.5分鐘）(圖11c) 不同，但兩者之質譜圖譜均出現質量爲43、107及164之特徵，惟 Scan No.186之質譜中已無質量爲206之克蠅原物質（圖11c）。因206與164之質量差數爲42，恰爲脫去一個乙酸根（acetyl group）之質量，故推測此分解物應爲脫乙酸根之克蠅產物（deacetylated cuelure, p-phenyl-2-butanone）。

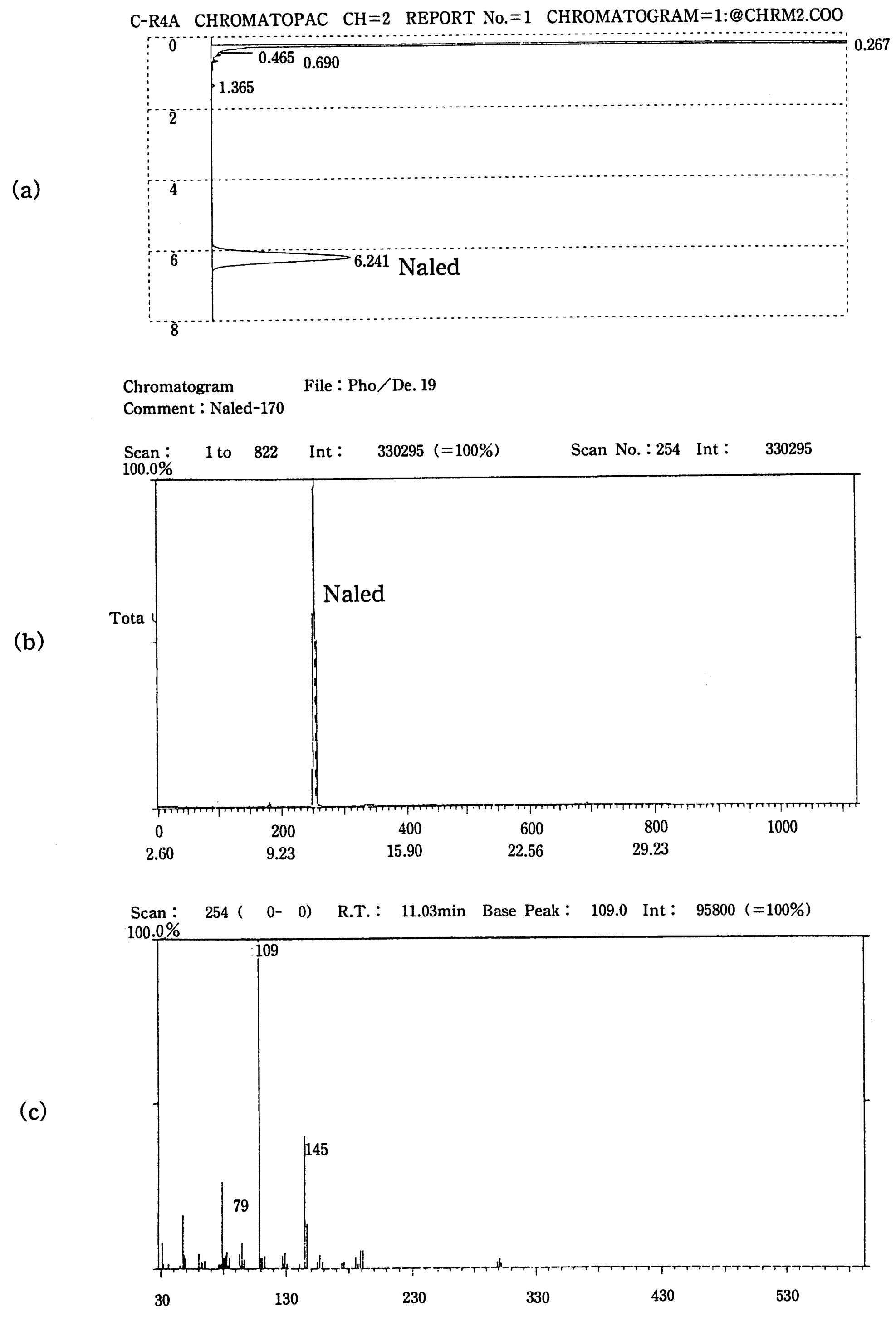


圖1. 乃力松標準品之 GC-FID (a) 與 GC-MS (b及c) 分析圖譜

Fig. 1. Gas chromatograph/FID (a) and GC-mass spectrum (b & c) of naled.

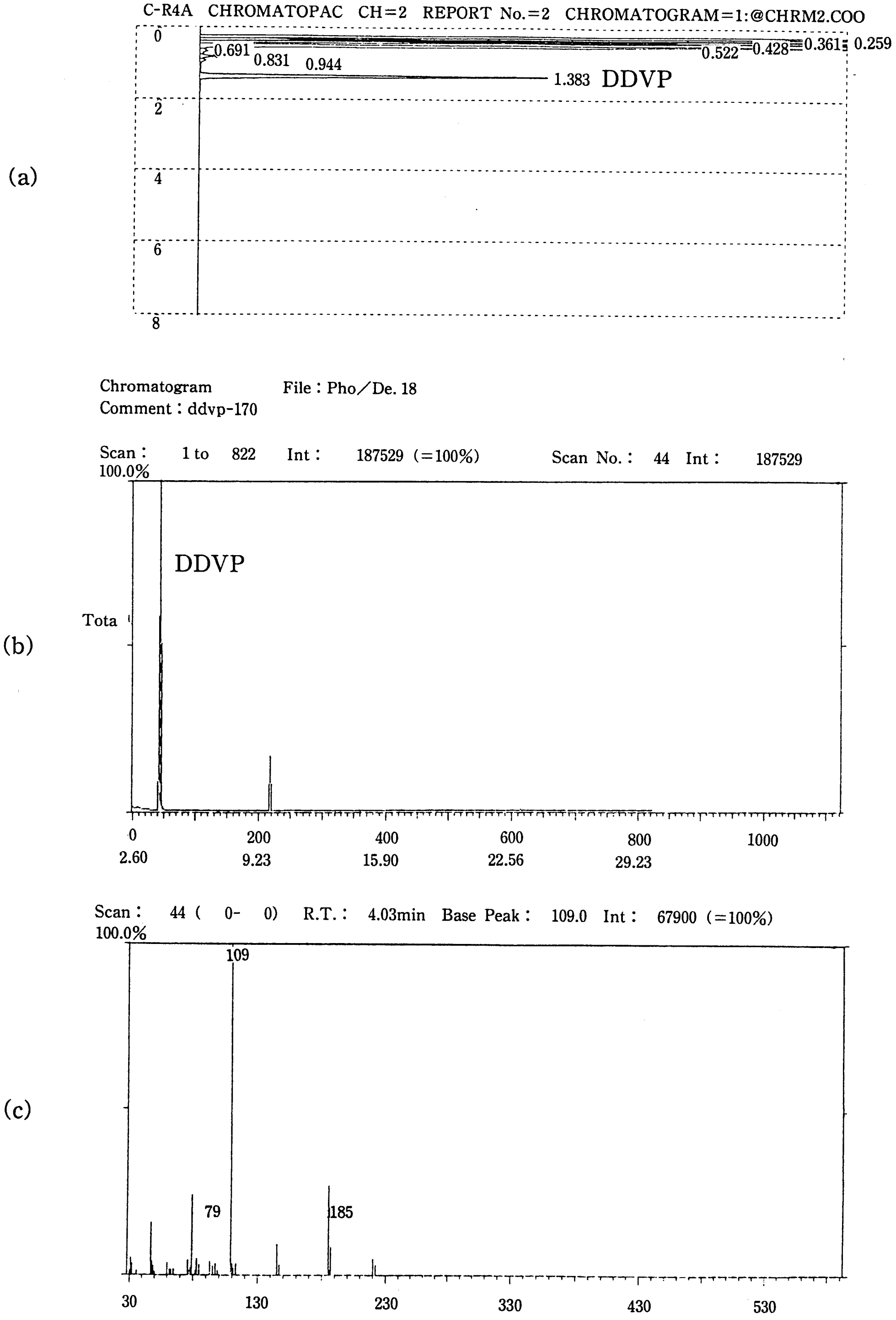


圖2. 二氯松標準品之 GC-FID (a) 與 GC-MS (b及c) 分析圖譜

Fig. 2. Gas chromatograph/FID (a) and GC-mass spectrum (b & c) of DDVP.

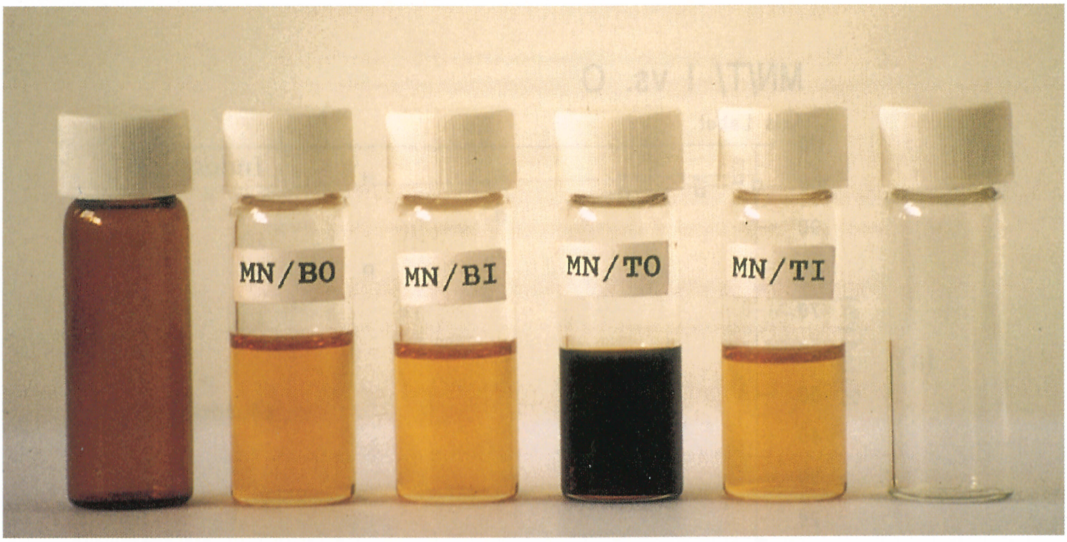


圖3. 果實蠅誘殺劑在不同環境下藥液褐變情形
(由左至右：茶色瓶室外，茶色瓶室內，透明瓶室外，透明瓶室內)

Fig. 3. Decomposition of fruit fly poison bait in different treatments
(from left to right：MN/BO, MN/BI, MN/TO,MN/TI) .
(M：methyl eugenol, N：naled, B：brown bottle, T：transparent bottle,
O：outdoor, I：indoor) .

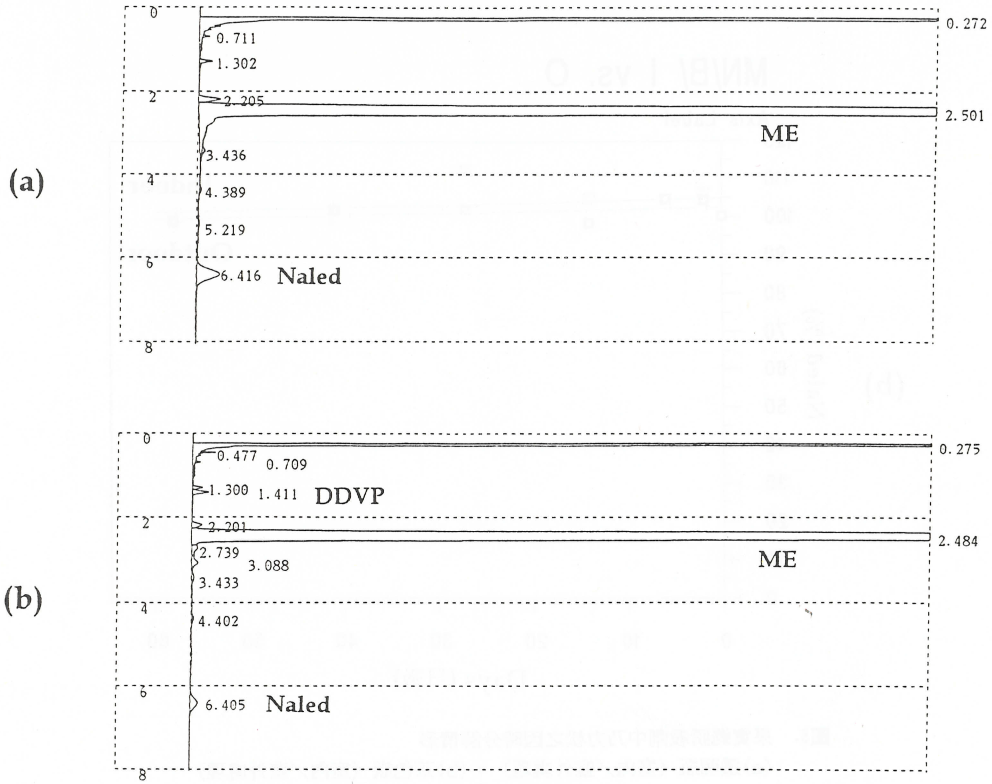
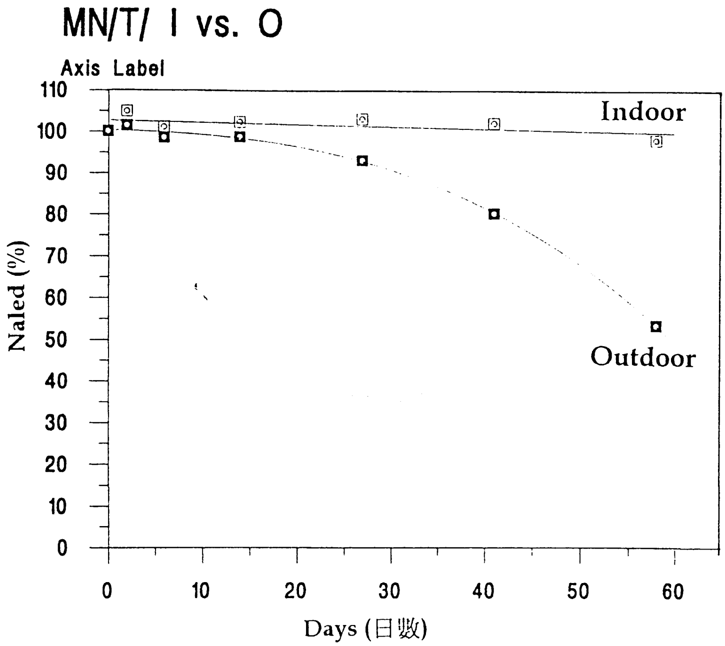


圖4. 果實蠅誘殺劑主成份及其分解物之 GC-FID 分析結果(a)第 0 天，(b)第58天

Fig. 4. Gas chromatographic analysis of fruit fly poison bait.(a)0 DAT, (b)58DAT.

(a)



(b)

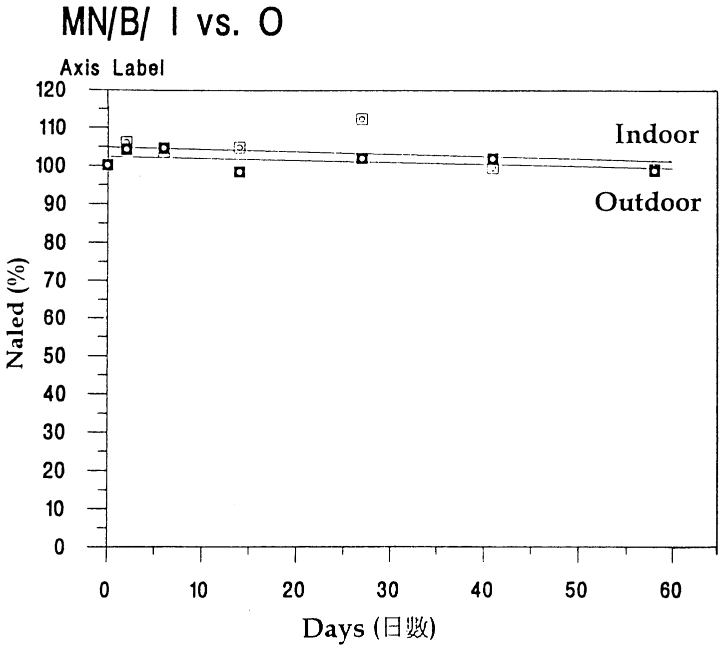


圖5. 果實蠅誘殺劑中乃力松之因時分解情形
(a)透明瓶（室內／室外處理），(b)茶色瓶（室內／室外處理）

Fig. 5. Decomposition of naled in fruit fly poison bait.
(a) transparent bottle (indoor vs. outdoor)
(b) brown bottle (indoor vs. outdoor)

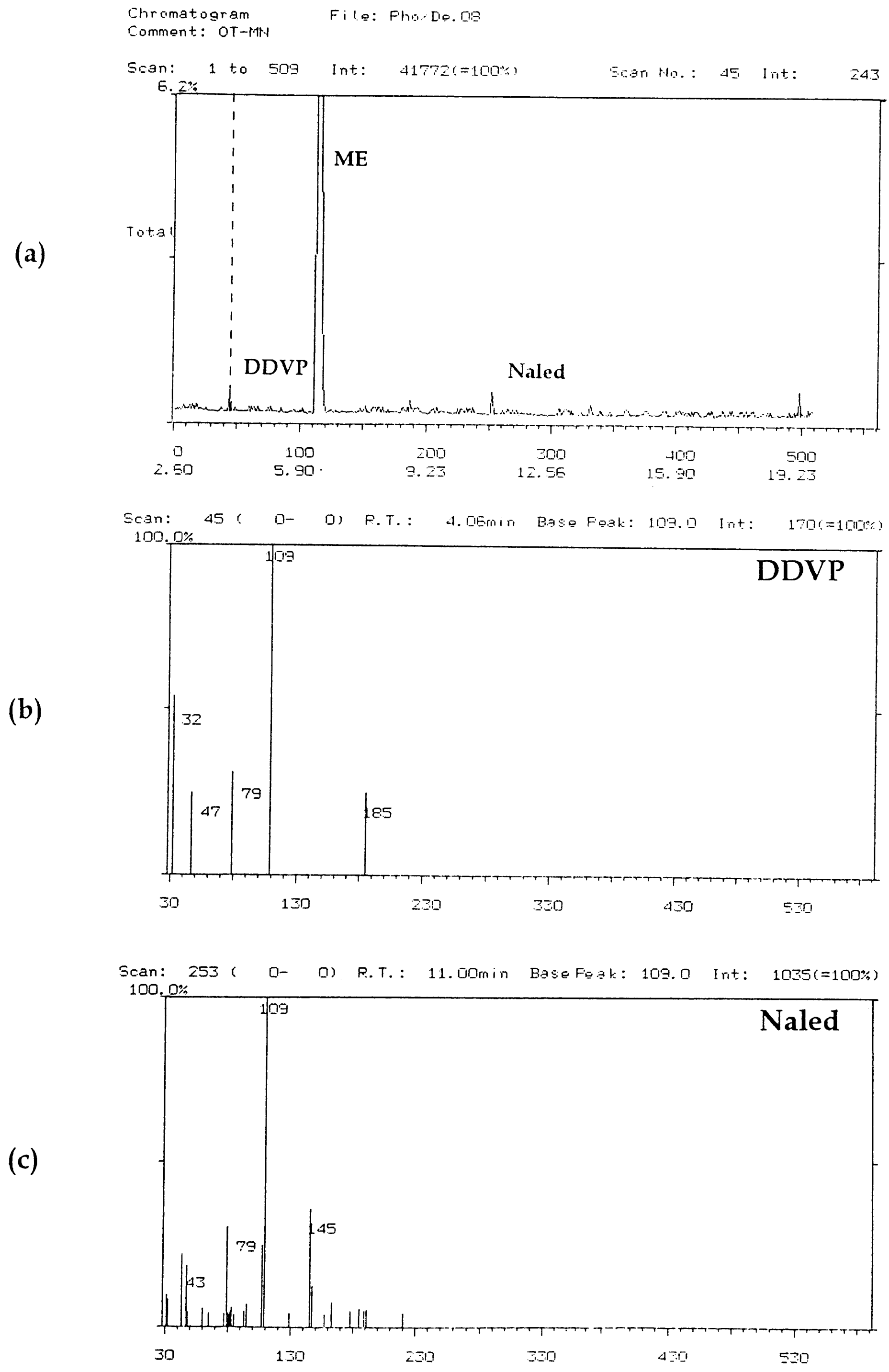


圖6. 第58天室外透明瓶裝果實蠅誘殺劑中乃力松及其分解物之色層分析(a)及質譜分析(b,c)

Fig. 6. Mass spectrum analysis of fruit fly poison bait after 58 days outdoor condition. (a)GC analysis; (b)mass spectrum of scan No. 45 (DDVP) of (a); (c)mass spectrum of scan No. 253 (Naled) of (a).

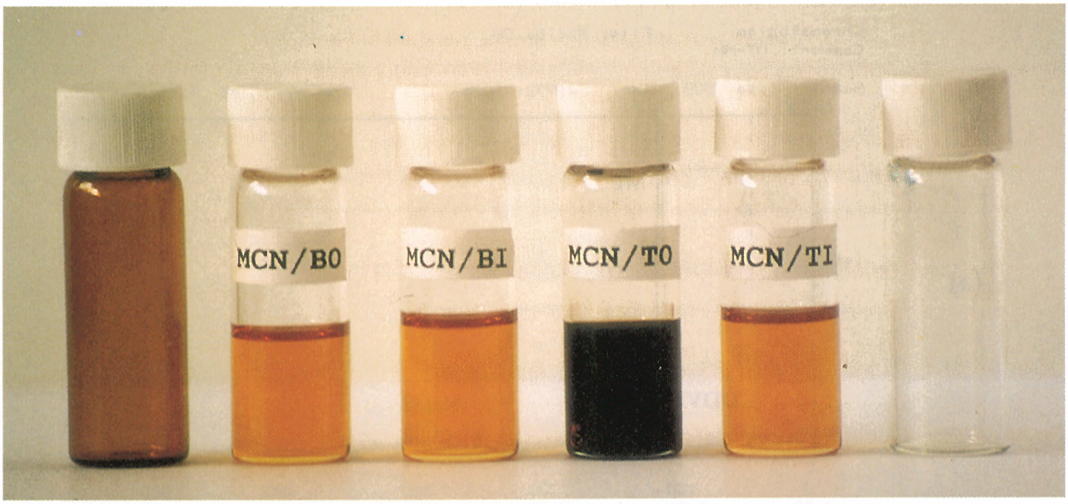


圖7. 瓜實蠅誘殺劑在不同環境下褐變情形
(由左至右：茶色瓶室外，茶色瓶室內，透明瓶室外，透明瓶室內)

Fig. 7. Decomposition of melon fly poison bait in different treatments (from left to right：MCN/BO, MCN/BI, MCN/TO, MCN/TI). (M：methyl eugenol, C：cuelure, N：naled, B：brown bottle, T：transparent bottle, O：outdoor, I：indoor).

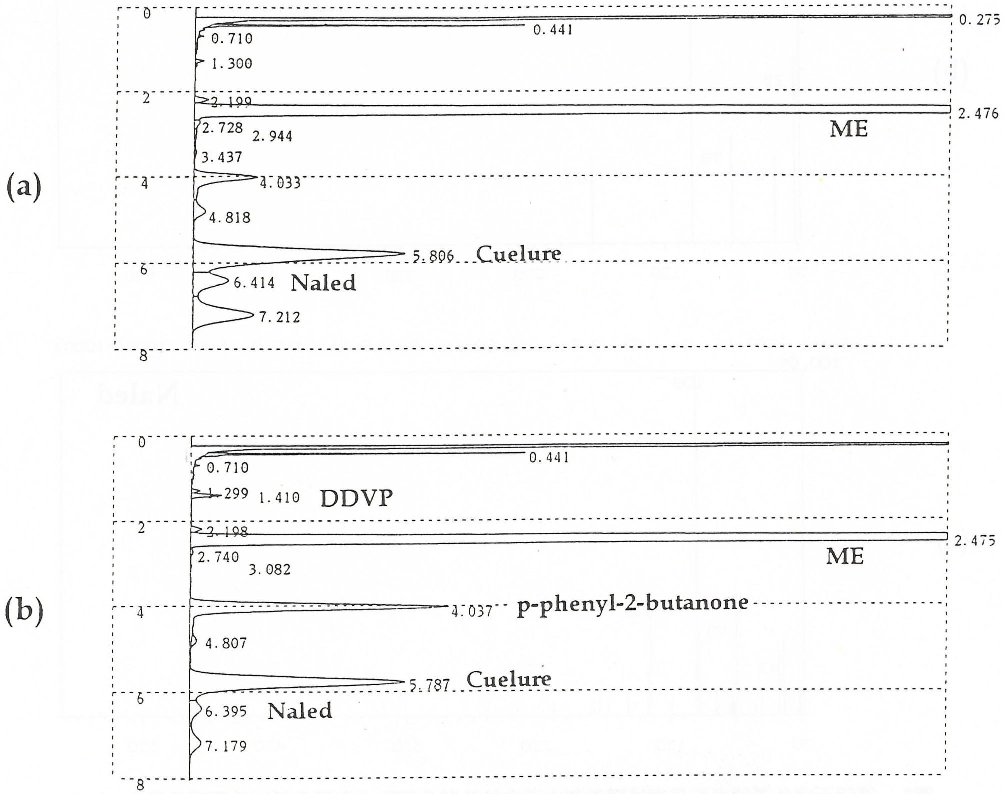
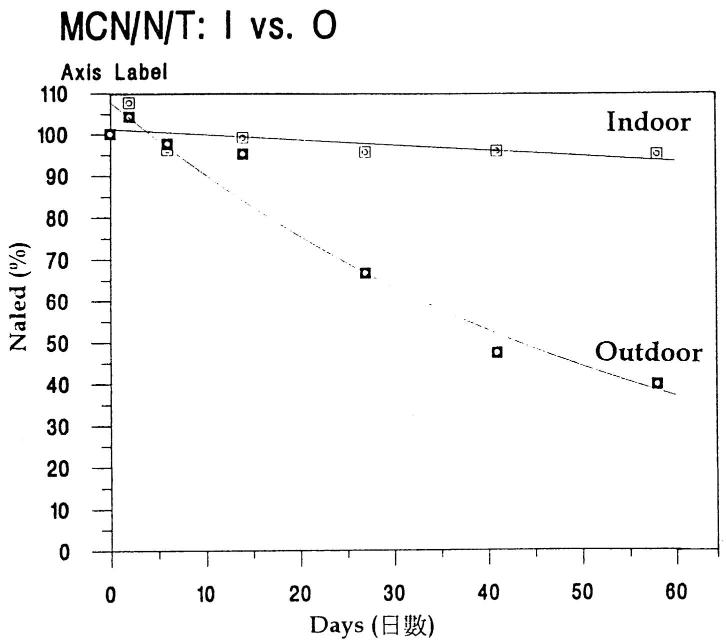


圖8. 瓜實蠅誘殺劑內克蠅、乃力松及其分解物之 GC-FID 分析圖。(a)第 0 天，(b)第 58 天

Fig. 8. Gas chromatography of melon fly poison bait to show the apparence of DDVP and p-phenyl-2-butanone. (a) 0 DAT, (b) 58DAT.

(a)



(b)

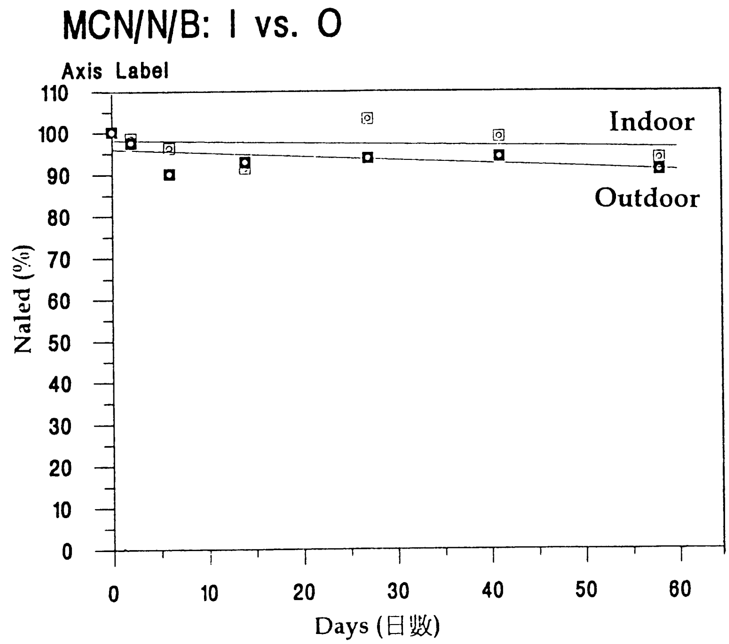
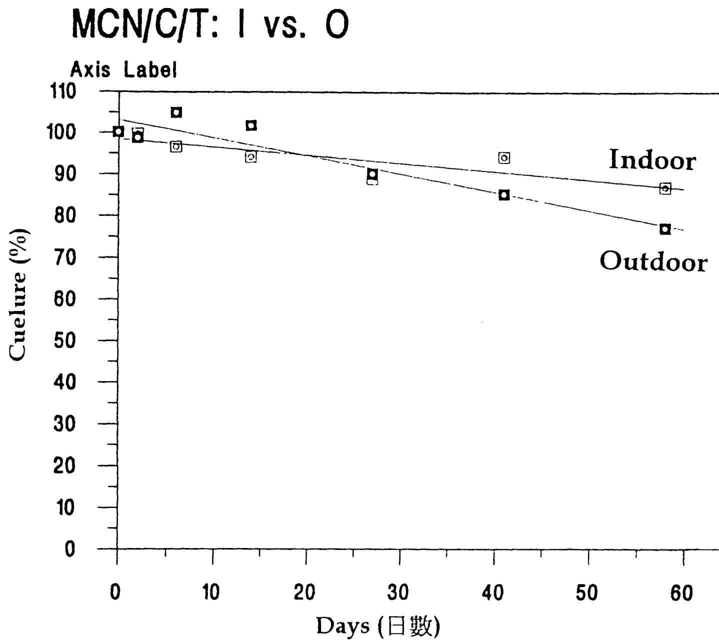


圖9. 瓜實蠅誘殺劑中乃力松之因時分解情形
(a)透明瓶（室內／室外處理），(b)茶色瓶（室內／室外處理）

Fig. 9. Decomposition of naled in melon fly poison bait.
(a) transparent bottle (indoor/outdoor)
(b) brown bottle (indoor/outdoor)

(a)



(b)

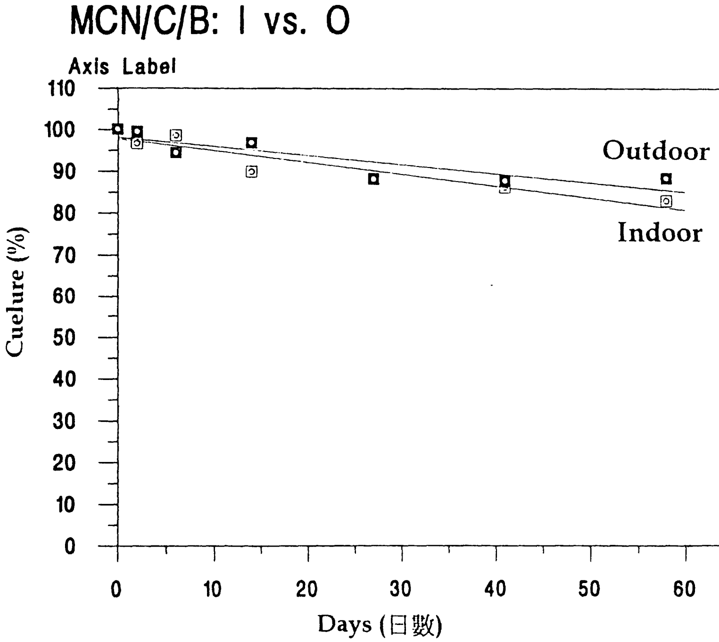


圖10. 瓜實蠅誘殺劑中克蠅之因時分解情形
(a)透明瓶（室內／室外處理），(b)茶色瓶（室內／室外處理）

Fig. 10. Decomposition of cuelure in melon fly poison bait.
(a) transparent bottle (indoor/outdoor)
(b) brown bottle (indoor/outdoor)

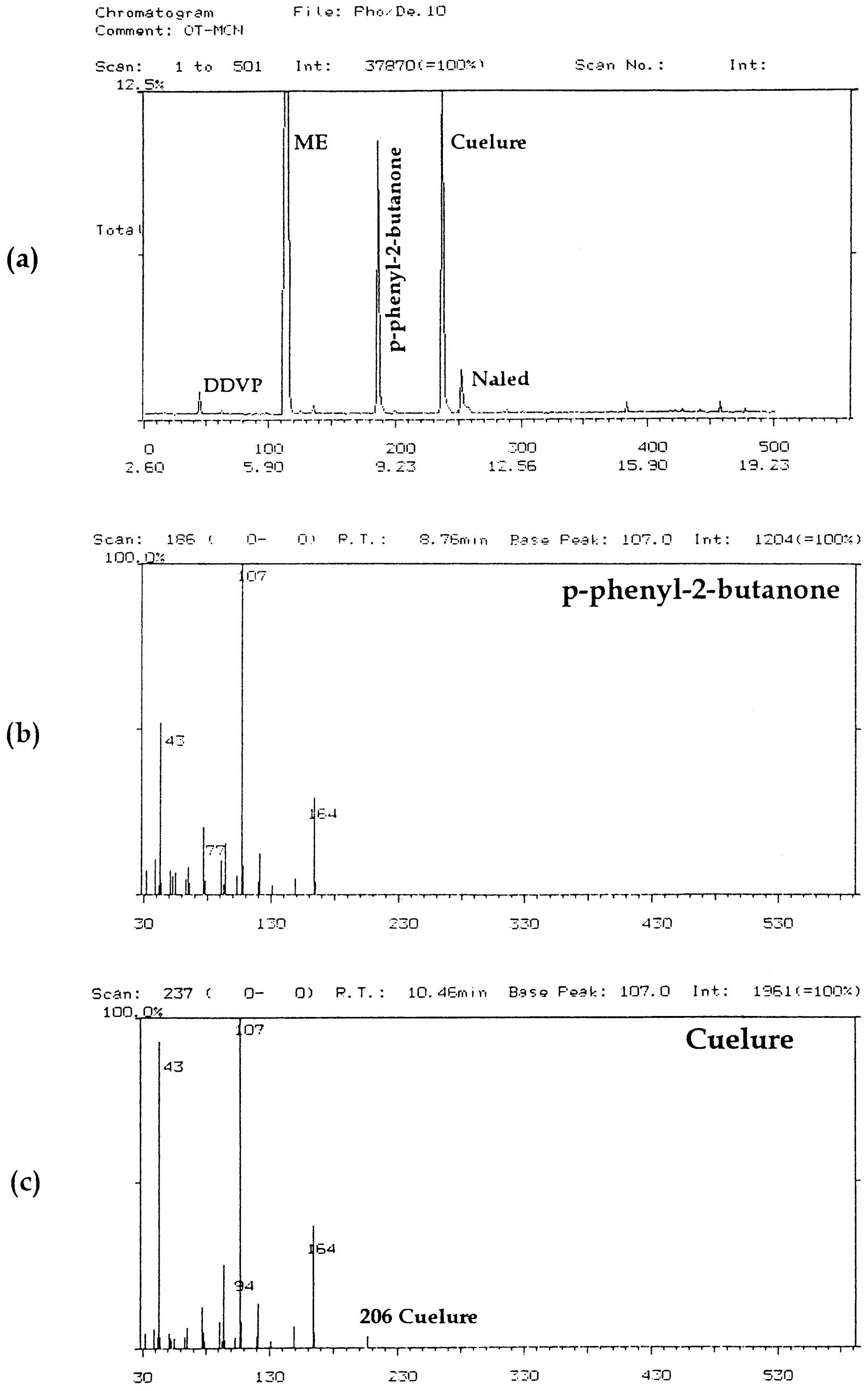


圖11. 第58天室外透明玻璃瓶處理瓜實蠅誘殺劑之質譜分析圖出現分解物，分別爲 DDVP 及 p-phenyl-2-butanone

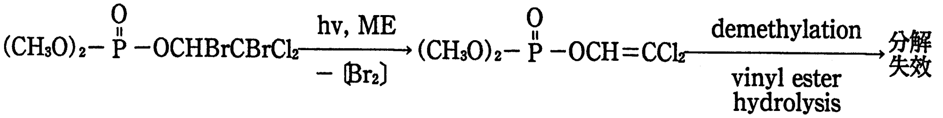
Fig. 11. Mass spectrum analysis of melon fly poison bait to show the apparence of DDVP and p-phenyl-2-butanone of transparent bottle in outdoor condition at 58 DAT.

討　論

用以誘殺果實蠅的含毒甲基丁香油會發生褐變之原因，顯然係乃力松溶於甲基丁香油介質中，易因紫外線照射而引起光分解作用（photolysis）。由於第58天之樣品中檢出約18%之二氯松存在，與尚未分解之35%乃力松之比率爲1：2，顯示二氯松是其分解途徑中之主要中間物。此一分解途徑爲先脫去兩個溴原子（Br_2）還原成爲二氯松，而解離之溴直接導致誘殺劑發生褐變，此與 Buchel[2]與Eto[3]所報導脫溴形成二氯松爲乃力松最常見的分解途徑相符，但此一經光分解之成因則尙未見諸於以往的報告之中。此外，是否甲基丁香油提供了更適合光分解的環境條件，則仍有待探討。而已消失的47%乃力松均已分解爲分子量更次於二氯松之物質，不但不具毒殺效果且已無法檢出，此應即1992～93年間，誘殺劑產生褐變而致藥效消退之原因。

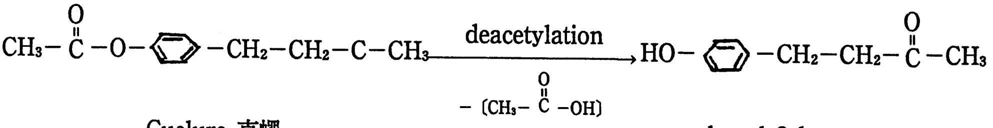
在相同光照及溫度環境條件下，以透明瓶包裝之誘殺劑置於室外時，乃力松急遽地變質，而同置於室外使用茶色瓶遮光之處理卻可大幅降低光解作用。就溫度因子而言，茶色瓶與透明瓶所放置之處所完全相同，因此，溫度應該與褐變無關。置於室內透明瓶中之誘殺劑分解情形亦極輕微，與室外之透明瓶包裝者顯著不同，由於室內光照與室外陽光之主要差異來自所含紫外線的強弱，因而推測陽光中的紫外線可能爲導致誘殺劑發生光解褐變之主因。使用遮光包裝，如鋁箔袋或茶色玻璃瓶，均可過濾紫外線，因而可提高果實蠅誘殺劑之保存期限。

克蠅之分解則與在此一試驗狀況下之光線或溫度差異均無相關，其脫去乙酸根的作用與常見之水解作用（hydrolysis）相似，應爲混合物相互作用，或由所含之不純物所引起之自然分解現象。因本試驗狀況與一般工廠配製瓜實蠅誘殺劑之室內環境相似，因此在配製誘殺劑時，克蠅成份之自發性分解應被列爲訂定誘殺劑有效期限之重要考慮因素。



(1)

Naled 乃力松　　DDVP 二氯松



(2)

Cuelure 克蠅　　p-phenyl-2-butanone

誌　謝

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Instability of the Currently Used Poison Baits for the Oriental Fruit Fly and Melon Fly —The Study on Decomposition of Naled and Cuelure[1]

Edward Yun Cheng[2], Te-Yeh Ku[3], Ching-Hua Kao[2] and Yu-Bin Huang[2]

Summary

The insecticide component naled, in methyl eugenol poison bait for oriental fruit fly (*Bactrocera dorsalis*), will easily decompose through dichlovos to non-toxic material by sunlight photolysis. Brown bottle packing of poison bait can prevent naled from decomposing by shading off the sunlight, hence stablize the formulation of this bait. Poison bait for control of melon fly (*Bactrocera cucurbitae*) contains cuelure, methyl eugenol and naled. The photo-decomposition of naled also occurred under sunlight in even faster rate than that of methyl eugenol-naled bait. The increase rate of decomposition may due to the mixing of more components in the bait. Brown bottle packing can also prevent the naled from decomposing. In the melon fly poison bait, 12~20% cuelure was deacetylated in a 2-month period, which was not affected by sunlight or temperature in the condition of this experiment. The loss of cuelure by autolysis should be specified for registering commercial formulation of melon fly poison bait.

Key words : Oriental fruit fly (*Bactrocera dorsalis* Hendel), Melon fly (*B. cucurbitae* Coguillett) , Poison bait, Photolysis.

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The Braconidae (Hymenoptera) of Taiwan
VII. Subtribe Triaspina[1]

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Abstract: The subtribe Triaspina (Hymenoptera: Braconidae: Helconinae: Brachistini) is revised for Taiwan. Three new species of the genus *Canalicephalus* Gibson and 22 new species of the genus *Triaspis* Haliday are described and illustrated in this paper. Keys to the genera and species of the Taiwanese Triaspina are also presented.

Key words : Triaspina, Helconinae, Braconidae, Taxonomy, Taiwan.

INTRODUCTION

The subtribe Triaspina (Hymenoptera: Braconidae: Helconinae: Brachistini) is characterized by the following combination of characters: vein r-m of forewing absent, vein m-cu of forewing antefurcal; first metasomal tergum immovably joined to T2, forming a rigid carapace with T3. The Triaspina contains 4 genera: *Canalicephalus* Gibson, *Dicyrtaspis* Van Achterberg, *Triaspis* Haliday and *Urosigalphus* Ashmead. About 290 species have been known worldwide. The members of the subtribe Triaspina of Taiwan are largely unknown and only one species, *Schizoprymnus imitatus* Papp, were reported to occur in this island. In this paper 25 new species are described from Taiwan. In the specimens examined only " in AEI" (=in American Entomological Institute) is indicated as the depository institution; where do not indicated the depository is Insect Collection of the Taiwan Agricultural Research Institute, Taichung, Taiwan, R.O.C.

In the sections of specimens examined, the following abbreviations are used for the collectors: BHC (B.H. Chen), CCC (C.C. Chen), CCCh (C.C. Chien), CCP (C.C. Pang), CHW (C.H. Wang), CHY (C.H. Yang), CJL (C.J. Lee), CNL (C.N. Lin), CYW (C.Y. Wong), HT (Henry Townes), KCC (K.C. Chou), KSL (K.S. Lin), LYC (L.Y. Chou), SCL (S.C. Lin), TL (T. Lin), and WST (W.S. Tang).

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The complete information for the collecting sites which used in the specimens examined section under each species are as follows:

CHIAYI: Alishan 2,400m.

HUALIEN: Tayuling 2,560m.

NANTOU: Lienhuachih 650m, Lushan 1,000m, Meifeng 2,150m, Sungkang 2,100m, Tsuifeng 2,300m, Tungpu 1,200m, Wushe 1,150m.

TAICHUNG: Anmashan 2,275m, Kukuan 730m, Wanfeng, Wufeng, Wuling 1,900m.

TAITUNG: Lanyu.

TERMINOLOGY

The terminology used here mainly follow Huber and Sharkey[10], Gauld and Bolton[8], and Van Achterberg[1] with additions and modifications. Descriptions of sculpture are largely based on Harris[9]. Some of these terms are explained as follows:

Collar: the more or less raised, anteroventral margin of the pronotum, just behind the head. The collar crosses the dorsal aspect of the pronotum and extends ventrally and posteriorly[17].

Coriaceous: mesh-like pattern in which the cells are flat and distinguished from each other by fine, impressed lines[6].

Flagellomere (F1, F2…): any flagellar segment of antenna.

Frontal line or carina: median groove or carina leading, when complete, from anterior ocellus to toruli[4].

Frontal depression: depressed area of frons behind each torulus[3].

Intertentorial line: shortest distance between anterior tentorial pits.

OD: diameter of ocellus, maximal diameter of a posterior ocellus[11].

Reticulate: mesh-like pattern in which the cells are shallowly concave so as to be separated by ridges[6].

Striate-punctate: with rows of punctures.

Subalar fossa: depressed area of mesopleuron beneath subalar prominence[4]. Van Achterberg[1] use the term, epicnemia area.

Temple: an area of the gena between the comound eye and the occipital carina.

Tentorial index: tentorio-ocular line over intertentorial line[16].

Tentorio-ocular line: shortest distance between anterior tentorial pit and eye.

Tergum (T1, T2,…): a dorsal sclerite of a body segment, which may be subdivided into tergites; specifically used for the metasoma[10].

Vein length: measured from the center of one juncture to the center of the next[17].

Key to genera and subgenera of the subtribe Triaspina from Taiwan

1. Vein M+Cu of forewing distinctly curved; transscutal articulation distinct ……………… *Canalicephalus* Gibson

-. Vein M+Cu of forewing nearly straight; transscutal articulation not developed ……………… *Triaspis* Haliday…2

2. Carapace distinctly segmented, definitely with 3 terga ······ *Triaspis* (*Triaspis*) Haliday
-. Carapace not segmented, or with sutures only weakly developed ································ *Triaspis* (*Schizoprymnus*) Foerster

Genus *CANALICEPHALUS* Gibson

Canalicephalus Gibson, 1977. Pac. Ins. 17: 241. Type species: *Canalicephalus orientalis* Gibson, original designation.

The genus *Canalicephalus* is characterized by the following combination of characters: vertex deeply notched; frons laterally without a pair of punctate tubercles; frontal carina distinct; frontal depression deep, glabrous; transscutal articulation distinct; vein M+Cu of forewing distinctly curved; outer hind tarsal claw similar in size to inner claw, carapace completely without sutures. It contains 4 species in the world. In this paper 3 new species are described from Taiwan.

Key to species of the genus *Canalicephalus* from Taiwan

1. Ovipositor sheath 0.41 times as long as forewing; carapace smooth apically and apicoventrally, without groove apicoventrally ······································ *longus* sp. n.
-. Ovipositor sheath 0.23-0.30 times as long as forewing; carapace rugose apically and apicoventrally, with or without groove apicoventrally ·· 2
2. Carapace with distinct groove apicoventrally; frons rugose-reticulate ········· *fugou* sp. n.
-. Carapace without distinct groove apicoventrally; frons densely punctate ······································· *taiwanensis* sp. n.

Canalicephalus fugou sp. n.

(Figs. 11, 35, 59, 85, 113, 137, 163, 189, 215, 241)

Female: Head: 2.0 times as wide as long and 1.3 times wider than mesonotum. Eye 2.8 times as long as temple. Temple densely punctate; frons rugose-reticulate; vertex reticulate. POL: OD: OOL=1: 0.41: 0.97. Face 0.49 times as high as wide and 1.5 times as wide as eye height and 0.64 times as wide as head, rugose-reticulate; cypeus rugose. Tentorial index 1.2. Malar space 1.6 times basal width of mandible. Antenna 17-segmented; F1 1.1 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.0, 2.9 and 1.1 times their width, respectively.

Mesosoma: 1.4 times as long as high. Pronotal side reticulate, dorsally densely setae. Notauli deep and crenulate; mesoscutum densely, shallowly punctate, rather rugulose anteriorly, middle lobe foveate posteriorly; scutellum puncticulate. Subalar fossa punctate, weakly crenulate; precoxal sulcus shallowly depressed, reticulate; anterior border and posteroventrally of mesopleuron punctulate; disc of mesopleuron smooth. Metapleuron reticulate. Propodeum reticulate-rugose; with median longitudinal carina anteriorly and with medioposterior area.

Wings: Forewing: stigma 2.4 times as long as wide; basal posterior section of stigma 1.4

times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 6.4: 1.7; m-cu: 2/Rs+M=1.1: 1; lcu-a postfurcal, 1/Cu: 2/Cu=0.32: 1. Hindwing: r-m: 1/M=0.33: 1; 1/M: Cu&cu-a=1.3: 1.

Hind leg: Coxa largely smooth. Lengths of femur, tibia and basitarsus 2.7, 4.7 and 3.5 times their width, respectively; tibia 1.1 times as long as femur; inner and outer spurs of tibia 0.50 and 0.42 times as long as basitarsus, respectively.

Metasoma: 2.0 times as long as wide; costate, interspace strigulate, with distinct groove apicoventrally. Dorsal carinae disinct basally. Ovipositor sheath 0.30 times as long as forewing.

Color: Black; palpi brownish yellow, mandible (apex dark brown) yellowish brown, tegula dark brown. Antenna yellowish brown basally, dark brown apically. Wings hyaline, stigma and veins dark brown. Legs yellowish brown; hing tibia and tarsus dark brown. Ovipositor sheath dark brown.

Lengths: Body 3.6 mm, antenna 2.3 mm, forewing 3.0 mm, ovipositor sheath 0.88 mm.

Male: Unknown.

Holotype: ♀, Tungpu, 20-22.VI.1980 (CCC).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species is close to *C. taiwanensis* sp. n., but differs from it by the middle lobe of mesoscutum foveate posteriorly, carapace with distinct groove apicoventrally and the frons rugose-reticulate.

Etymology: The specific name is the Chinese noun "fugou" (ventral groove). It refers to the carapace with distinct groove apico-ventrally.

Canalicephalus longus sp. n.

(Figs. 12, 36, 60, 86, 114, 138, 164, 190, 216, 242)

Female: Head: 1.9 times as wide as long and 1.2 times wider than mesonotum. Eye 4.6 times as long as temple. Temple densely punctate; frons punctate-reticulate, rugose ventrally; vertex densely punctate. POL: OD: OOL=1: 0.39: 0.61. Face 0.53 times as high as wide and 1.3 times as wide as eye height and 0.59 times as wide as head, rugose-reticulate; cypeus rugose-reticulate. Tentorial index 1.3. Malar space 1.4 times basal width of mandible, rugose. Antenna 17-segmented; F1 0.90 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.8, 4.2 and 1.7 times their width, respectively.

Mesosoma: 1.5 times as long as high. Pronotal side reticulate, dorsally densely setae. Notauli deep and crenulate; mesoscutum densely, shallowly punctate, middle lobe foveate posteriorly; scutellum puncticulate. Subalar fossa punctulate, precoxal sulcus crenulate; anterior border and posteroventrally of mesopleuron puntulate; disc of mesopleuron smooth. Metapleuron largely reticulate, rather smooth dorsally. Propodeum reticulate-rugose; with median longitudinal carina anteriorly and transverse carina, without medioposterior area.

Wings: Forewing: stigma 2.4 times as long as wide; basal posterior section of stigma 1.4

times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 5.9: 1.5; m-cu: 2/Rs+M=1.1: 1; lcu-a postfurcal, 1/Cu: 2/Cu=0.31: 1. Hindwing: r-m: 1/M=0.55: 1; 1/M: Cu&cu-a =1.2: 1.

Hind leg: Coxa largely smooth. Lengths of femur, tibia and basitarsus 3.1, 5.6 and 3.9 times their width, respectively; tibia 1.1 times as long as femur; inner and outer spurs of tibia, 0.52 and 0.45 times as long as basitarsus, respectively.

Metasoma: 1.8 times as long as wide; costate, interspace strigulate, rather smooth apically and apicoventrally, without groove apicoventrally. Dorsal carinae distinct basally. Ovipositor sheath 0.41 times as long as forewing.

Color: Black; palpi yellowish brown, tegula dark brown. Antenna yellowish brown basally, dark brown apically. Wings hyaline, stigma and veins dark brown. Legs yellowish brown; hing tibia and tarsus brown. Ovipositor sheath dark brown.

Lengths: Body 3.9 mm, antenna 2.9 mm, forewing 3.2 mm, ovipositor sheath 1.3 mm.

Male: Unknown.

Holotype: ♀, Tungpu, 23-27.VII.1984 (KCC & CHY).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species differs from the other Taiwanese *Canalicephalus* species by the ovipositor sheath about 0.4 times as long forewing; carapace smoth apically and apicoventrally, without groove apicoventrally.

Etymology: *Longus* means long in Latin, refers to its ovipositor sheath rather longer.

Canalicephalus taiwanensis sp. n.

(Figs. 13, 37, 61, 87, 115, 139, 165, 191, 217, 243)

Female: Head: 2.0 times as wide as long and 1.2 times wider than mesonotum. Eye 3.9 times as long as temple. Temple, frons and vertex densely punctate. POL: OD: OOL=1: 0.46: 0.81. Face 0.55 times as high as wide and 1.3 times as wide as eye height and 0.59 times as wide as head, reticulate to rugose-reticulate; clypeus rugulose-reticulate. Tentorial index 1.2. Malar space 1.3 times basal width of mandible, rugulose-reticulate. Antenna 17-segmented; F1 1.1 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.0, 2.8 and 1.3 times their width, respectively.

Mesosoma: 1.4 times as long as high. Pronotal side reticulate, dorsally densely setae. Notauli deep and crenulate; mesoscutum punctulate, punctures larger posteriorly; scutellum sparsely punctate. Subalar fossa weakly crenulate; precoxal sulcus reticulate, disc of mesopleuron largely smooth, sparsely punctate posteroventrally. Metapleuron reticulate. Propodeum reticulate-rugose; with median longitudinal carina anteriorly and shortly developed transverse carina, without medioposterior area.

Wings: Forewing: stigma 2.3 times as long as wide; basal posterior section of stigma 1.3 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 5.6: 1.5; m-cu: 2/Rs+M=1.2: 1; lcu-a postfurcal, 1/Cu: 2/Cu=0.30: 1. Hindwing: r-m: 1/M=0.45: 1; 1/M: Cu&cu-a=1.1: 1.

Hind leg: Coxa largely smooth. Lengths of femur, tibia and basitarsus 2.8, 4.4 and 3.7 times their width, respectively; tibia 1.1 times as long as femur; inner and outer spurs of tibia, 0.59 and 0.50 times as long as basitarsus, respectively.

Metasoma: 1.9 times as long as wide; costate, interspace strigulate, without distinct groove apicoventrally. Dorsal carinae disinct basally. Ovipositor sheath 0.23 times as long as forewing.

Color: Black; palpi yellowish brown, tegula blackish brown. Antenna yellowish brown basally, dark brown apically. Wings hyaline, stigma and veins dark brown. Legs yellowish brown; hing tibia (except basally) and tarsus dark brown. Ovipositor sheath dark brown.

Lengths: Body 3.3 mm, antenna 2.1 mm, forewing 2.7 mm, ovipositor sheath 0.63 mm.

Male: Similar to female.

Holotype: ♀, Lienhuachih, VIII.1984 (KCL & KCC). Paratypes: Lienhuachih, 1 ♀, same data as holotye. Tungpu, 1♂, 23-27.VII.1984 (KCC & CHY).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species is close to *C. fugou* sp. n., but differs from it by the middle lobe of mesoscutum punctate posteriorly, carapace without distinct groove apicoventrally, frons densely punctate.

Etymology: The specific name is derived from Taiwan.

Genus *TRIASPIS* Haliday

Triaspis Haliday, 1835. Ent. Mag. 3: 124, as subgenus of *Helcon.* Type species: *Sigalphus caudatus* Nees; designated by Viereck, 1912. - Viereck, 1912. Proc. U.S. natn. Mus. 42: 628. - Martin, 1956. Publs. Dep. Agric. Can. 965: 61. - Mason, 1974. Proc. Entomol. Soc. Wash. 76(3): 245. - Papp, 1984. Acta Zool. Hung. 30(1-2): 139.

Schizoprymnus Foerster, 1862. Verh. naturh. Ver. preuss. Rheinl. 19: 242. Type species: *Sigalphus obscurus* Nees, by monotypy and original designation.

Ichneutipterus Vachal, 1907. Revue Ent. 26: 122. Type species: *Sigalphus* ? *ichneutipterus* Vachal, by monotypy.

Muiriella Fullaway 1919. J. Straits Brch R. asiat. Soc. 80: 47. Type species: *Muiriella concisa* Fullaway, by monotypy and original designation.

Fahringer[7] placed *Schizoprymnus* Foerster as a subgenus of *Triaspis* Haliday and this is followed by De Saeger[5] and Martin[12]. However, Papp[13-15] and Belokobylskij[2] treated them as separate genera. Papp[13] considered *Muiriella* Fullaway as a subgenus of *Schizoprymnus.* The authors consider *Schizoprymnus* and *Muiriella* as subgenera of *Triaspis* in this paper.

The genus *Triaspis* is characterized by the following combination of characters: vertex without notched; frons laterally without a pair of punctate tubercles; transscutal articulation not developed; vein M+Cu of forewing nearly straight; outer hind tarsal claw similar in size to inner claw; carapace completely without sutures, or with distinct sutures. It

contains about 200 species in the world. In this paper 22 new species are described from Taiwan.

Subgenus SCHIZOPRYMNUS Foerster

Schizoprymnus Foerster, 1862. Verh. naturh. Ver. preuss. Rheinl. 19: 242. Type species: *Sigalphus obscurus* Nees, by monotypy and original designation. - Gibson, 1972. Misc. Publ. Entomol. Soc. Amer. 8: 85. - Papp, 1984. Acta Zool. Hung. 30(1-2): 138.

Triaspis (*Schizoprymnus*): Fahringer, 1934. Opusc. bracon 3(5-8): 368. - Martin, 1956. Publs. Dep. Agric. Can. 965: 98.

The subgenus *Schizoprymnus* is characterized by the following combination of characters: propodeum without dinstict spines; carapace without sutures, or at most first suture between T1 and T2 more or less distinct, second suture between T2 and T3 effaced; rim of carapace behind usually not denticulate. It contains about 82 species in the world. In this Paper 20 new species are described from Taiwan.

Key to species of the subgenus *Schizoprymnus* from Taiwan

1. Rim of carapace behind weakly denticulate (Fig. 220) ······ *chouwen* sp. n.
-. Rim of carapace behind not denticulate (Fig. 221) ······ 2
2. T3 and precoxal sulcus completely smooth ······ *calvus* sp. n.
-. T3 weakly to strongly sculptured, at most smooth apically; precoxal at least weakly sculptured ······ 3
3. Frons with large lamellate frontal carina; ovipositor sheath 0.25 times as long as forewing ······ 4
-. Frons without large lamellate frontal carina; ovipositor sheath variable ······ 5
4. Frons rugulose-reticulate laterally; clypeus convex apically ······ *borpian* sp. n.
-. Frons punctulate laterally; clypeus almost straight apically ······ *lienhuachihensis* sp. n.
5. Carapace apicoventrally distinctly incurved ······ *imitatus* Papp
-. Carapace apicoventrally not or at most weakly incurved ······ 6
6. Vein 1/R1 of forewing shorter than or subequal to stigmal length ······ 7
-. Vein 1/R1 of forewing distinctly longer than stigmal length ······ 17
7. Clypeus concave apically, sharply pointed medially ······ 8
-. Clypeus almost straight to convex, not sharply pointed medially ······ 10
8. Metasoma 1.7 times as long as wide; carapace apicoventrally weakly incurved ······ *shan* sp. n.
-. Metasoma 1.3 times as long as wide; carapace apicoventrally almost not incurved ······ 9
9. Metasoma distinctly higher posteriorly than anteriorly (Fig. 194); antenna 23-segmented; metacoxa rugulose basally; vein 1/R1 of forewing almost as long as stigmal length ······ *hui* sp. n.
-. Metasoma indistinctly higher posteriorly than anteriorly (Fig. 192); antenna 19-segmented; metacoxa smooth basally; vein 1/R1 of forewing shorter than stigmal length ······ *chiu* sp. n.

10. Antenna 36-segmented; ovipositor sheath 0.65 times as long as forewing length .... *bicolor* sp. n.
-. Antenna 16-25-segmented; ovipositor sheath 0.27-0.48 times as long as forewing length 11
11. Apical rim of carapace almost not emarginated; ovipositor sheath 0.27 times as long as forewing length .... *plenus* sp. n.
-. Apical rim of carapace moderately to strongly emarginated or semicircular emarginated; ovipositor sheath 0.33-0.48 times as long as forewing length 12
12. Tentorial index 1.2; apical rim of carapace semicircular emarginated (Fig. 225) .... *loi* sp. n.
-. Tentorial index 0.5-0.6; apical rim of carapace moderately to strongly emarginated (Fig. 232) 13
13. Carinae on T1+T2 more straight and parallel (Fig. 177); metasoma 1.7 times as long as wide .... *ketiao* sp. n.
-. Carinae on T1+T2 less straight and parallel (Figs. 166, 171, 174, 175); metasoma 1.3-1.5 times as long as wide 14
14. Ovipositor sheath 0.33 times as long as forewing length .... *distinctus* sp. n.
-. Ovipositor sheath 0.44-0.48 times as long as forewing length 15
15. Metacoxa black .... *beitun* sp. n.
-. Metacoxa largely brownish yellow 16
16. Body black; metasoma 1.3 times as long as wide .... *robustus* sp. n.
-. Body dark brown: metasoma 1.5 times as long as wide .... *tungpuensis* sp. n.
17. Ovipositor sheath distinctly shorter than carapace 18
-. Ovipositor sheath distinctly longer than carapace 20
18. Metasoma in dorsal view constricted posteriorly (Fig. 176); tentorial index 0.64 .... *fessus* sp. n.
-. Metasoma in dorsal view rather round posteriorly (Figs. 170, 186); tentorial index 0.75-0.85 19
19. Clypeus distinctly rugose ventrally; precoxal sulcus rugose-reticulate ...... *chunji* sp. n.
-. Clypeus sparsely punctate ventrally; precoxal sulcus foveate .... *curvatus* sp. n.
20. Ovipositor sheath 0.55 times as long as forewing length; metasoma 1.2 times as long as wide; antenna 23-25-segmented .... *kueichia* sp. n.
-. Ovipositor sheath 0.69 times as long as forewing length; metasoma 1.5 times as long as wide; antenna 17-20-segmented .... *ovatus* sp. n.

Triaspis (Schizoprymnus) beitun sp. n.

(Figs. 28, 38, 62, 88, 116, 140, 166, 195, 235, 244)

Female: Head: 1.8 times as wide as long and 1.3 times wider than mesonotum. Eye 0.92 times as long as temple. Temple and vertex puncticulate; frons punctulate laterally, mediodorsally glabrous, medioventrally with curved carinae; without large lamellate frontal carina. POL: OD: OOL=1: 0.62: 1.7. Face 0.54 times as high as wide and 1.2 times as wide as eye height and 0.59 times as wide as head; punctulate, with rugae dorsally; clypeus

puncticulate, almost straight apically, not sharply pointed medially. Tentorial index 0.55. Malar space 0.86 times basal width of mandible. Antenna 21-23-segmented; F1 1.0 times as long as F2; lengths of F1, F2 and penultimate flagellomere 2.5, 2.5 and 1.4 times their width, respectively.

Mesosoma: 1.4 times as long as high. Pronotal side medially and anteroventrally more or less rugulose; rest largely smooth. Notauli deep and crenulate; mesoscutum punctulate, middle lobe rugulose posteriorly; scutellum puncticulate. Subalar fossa smooth with carinae; precoxal sulcus rugulose-reticulate; disc of mesopleuron glabrate. Metapleuron rather punctulate dorsally; rugulose-rugose ventrally Propodeum punctulate anteriorly, more or less rugulose-reticulate posteriorly; with median longitudinal carina anteriorly and transverse carina, without distinct medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 2.8 times as long as wide; 1/R1 almost as long as stigmal length; basal posterior section of stigma 1.1 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 8.8: 2.2; m-cu: 2/Rs+M=1.6: 1; lcu-a postfurcal, 1/Cu: 2/Cu=0.23: 1. Hindwing: r-m: 1/M=0.42: 1; 1/M: Cu&cu-a=2.4: 1.

Hind leg: Coxa rugulose dorsobasally. Lengths of femur, tibia and basitarsus 3.7, 7.1 and 4.7 times their width, respectively; tibia 1.4 times as long as femur; inner and outer spurs of tibia 0.50 and 0.43 times as long as basitarsus, respectively.

Metasoma: 1.4 times as long as wide; rugose-reticulate; apically not incurved. T1 0.68 times as long as wide apically; dorsal carinae disinct anteriorly; T2+T3 0.81 times as long as wide. Apical rim of carapace strongly emarginated. Ovipositor sheath 0.36 times as long as forewing.

Color: Black; palpi yellow, tegula dark briown. Antenna blackish brown. Wings hyaline, stigma and veins dark brown. Legs brown; coxae more or less black, hind tibia (except base) and tarsus dark brown. Ovipositor sheath blackish brown.

Lengths: Body 1.9 mm, antenna 1.7 mm, forewing 2.1 mm, ovipositor sheath 0.75 mm.

Male: Unknown.

Holotype: ♀, Sungkang, X.1985 (KSL). Paratypes: Anmashan, 1♀, 6-9.VII.1979 (LYC). Meifeng, 2♀, 15.VII.1982 (SCL & CNL); 1♀, 15.VII.1982 (SCL & CNL); 1♀, 4-7.X.1982 (KCC); Sungkang, 1♀, 13-15.IX.1984 (KSL & SCL).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species differs from the other Taiwanese *Triaspis* species by the following combination of characters: vein 1/R1 of forewing almost as long as stigmal length, frons glabrous mediodorsally, clypeus not sharply pointed medially, apical rim of carapace strongly emarginate, ovipositor sheath slightly longer than metasoma length, and the metacoxa black.

Etymology: The specific name is Chinese noun "beitun" (dorsal shield). It refers to the shape of metasoma.

Triaspis (*Schizoprymnus*) *bicolor* sp. n.

(Figs. 18, 39, 63, 89, 117, 141, 167, 196, 227, 245)

Female: Head: 1.8 times as wide as long and 1.2 times wider than mesonotum. Eye 1.2 times as long as temple. Temple rather densely punctate. Frons rugose-reticulate; without large lamellate frontal carina. POL: OD: OOL=1: 0.70: 1.9. Vertex rugose-reticulate between ocelli and eye, rather densely punctate posterad ocelli. Face 0.49 times as high as wide and 1.4 times as wide as eye height and 0.63 times as wide as head, rugose; clypeus largely rugose, rather smooth ventrally, convex apically, not sharply pointed medially. Tentorial index 0.83. Malar space 0.73 times basal width of mandible. Antenna 36-segmented; F1 1.0 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.5, 3.5 and 1.5 times their width, respectively.

Mesosoma: 1.5 times as long as high. Pronotal side medially and reticulate, dorsoposteriorly foveate, rest largely smooth. Notauli deep and crenulate; mesoscutum rather densely punctate, middle lobe foveate posteriorly; scutellum puncticulate. Subalar fossa densely punctate, with carinae posteriorly; precoxal sulcus crenulate; disc of mesopleuron rather densely punctate. Metapleuron rugose-reticulate. Propodeum rugose-reticulate; with median longitudinal carina and transverse carina, with wide medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 2.6 times as long as wide; 1/R1 almost as long as stigmal length; basal posterior section of stigma 1.3 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 8.0: 2.8; m-cu: 2/Rs+M=1.1: 1; lcu-a postfurcal, 1/Cu: 2/Cu=0.26: 1. Hindwing: r-m: 1/M=0.67: 1; 1/M: Cu&cu-a=1.7: 1.

Hind leg: Coxa smooth. Lengths of femur, tibia and basitarsus 3.7, 8.3 and 5.3 times their width, respectively; tibia 1.4 times as long as femur; inner and outer spurs of tibia 0.47 and 0.41 times as long as basitarsus, respectively.

Metasoma: 1.6 times as long as wide; rugose-reticulate; apically not incurved. T1 0.66 times as long as wide apically; dorsal carinae disinct in basal 0.8; T2+T3 1.0 times as long as wide. Apical rim of carapace strongly emarginated. Ovipositor sheath 0.65 times as long as forewing.

Color: Black; palpi blackish brown, pronotum, mesonotum, anterodorsal area of mesopleuron and tegula reddish borwn. Antenna blackish brown. Wings hyaline, stigma and veins dark brown. Legs blackish brown. Ovipositor sheath blackish brown.

Lengths: Body 4.3 mm, antenna 4.3 mm, forewing 4.2 mm, ovipositor sheath 2.8 mm.

Male: Unknown.

Holotype: ♀, Meifeng, XII.1984 (KSL & KCC). Paratypes: Sungkang, 1♀, X.1984 (KSL & KCC).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species is close to *Schizoprymnus commotus* Papp, 1989, but differs from it by the shape of carapace in lateral view.

Etymology: The specific name refers to its body with black and reddish brown coloration.

Triaspis (*Schizoprymnus*) *borpian* sp. n.

(Figs. 17, 40, 64, 90, 118, 142, 181, 206, 223, 246)

Female: Head: 1.6 times as wide as long and 1.3 times wider than mesonotum. Eye 1.0 times as long as temple. Temple punctulate. POL: OD: OOL=1: 0.56: 2.0. Frons rugulose-reticulate laterally; with large lamellate frontal carina; frontal depression rugulose-rugose. Vertex rugulose-reticulate around ocelli. Face 0.47 times as high as wide and 1.5 times as wide as eye height and 0.63 times as wide as head, rugulose; clypeus faintly rugulose, convex apically, not sharply pointed medially. Tentorial index 1.3. Malar space 1.5 times basal width of mandible. Antenna 25-26-segmented; F1 0.94 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.3, 3.4 and 1.1 times their width, respectively.

Mesosoma: 1.6 times as long as high. Pronotal side rugose-reticulate ventrally, punctulate dorsally. Notauli deep and crenulate; middle lobe of mesoscutum faintly rugulose, sculptures along notauli rather stronger; lateral lobes of mesoscutum puctulate; scutellum faintly rugulose. Subalar fossa crenulate to rugose; precoxal sulcus rugose-reticulate; disc of mesopleuron faintly rugulose to rugose. Metapleuron rugose-reticulate. Propodeum rugose-reticulate; with median longitudinal carina, without transverse carina and medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 2.8 times as long as wide; 1/R1 shorter than stigmal length; basal posterior section of stigma 1.5 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 6.6: 2.3; m-cu: 2/Rs+M=1.3: 1; lcu-a intertial. Hindwing: r-m: 1/M=0.50: 1; 1/M: Cu&cu-a=1.7: 1.

Hind leg: Coxa rugulose dorsobasally. Lengths of femur, tibia and basitarsus 4.8, 9.3 and 7.0 times their width, respectively; tibia 1.5 times as long as femur; inner and outer spurs of tibia 0.29 and 0.24 times as long as basitarsus, respectively.

Metasoma: 2.1 times as long as wide; rugose-reticulate; apicoventrally distinctly incurved. T1 0.73 times as long as wide apically; dorsal carinae rather disinct in basal 0.3; T2+T3 1.4 times as long as wide. Apical rim of carapace semicircularly emarginated. Ovipositor sheath 0.23 times as long as forewing.

Color: Black; palpi brown, tegula dark brown. Antenna dark brown. Wings hyaline, stigma and veins dark brown. Legs brown. Ovipositor sheath blackish brown.

Lengths: Body 3.6 mm, antenna 3.0 mm, forewing 3.1 mm, ovipositor sheath 0.73 mm.

Male: Unknown.

Holotype: ♀, Tsuifeng, 23-25.VI.1983 (KSL & SCL). Paratypoes: Tsuifeng, 2♀, 23-25. VI.1983 (KSL & SCL); 2♀, 5.VIII.1984 (KSL); Tungpu, 1♀, 23-27. VII. 1984 (KCC & CHY).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species is close to *T. lienhuachihensis* sp. n., but differs from it by the frons rugulose-reticulate laterally and the clypeus convex apically.

Etymology: The specific name is Chinese noun "borpian" (lamella). It refers to the frons with a lamella medially.

Triaspis (*Schizoprymnus*) *calvus* sp. n.

(Figs. 29, 65, 91, 119, 143, 180, 208, 219, 247)

Female: Head: 1.7 times as wide as long and 1.3 times wider than mesonotum. Eye 0.97 times as long as temple. Temple, frons (except medially glabrous) and vertex punctulate; without large lamellate frontal carina. POL: OD: OOL=1: 0.59: 1.6. Face 0.58 times as high as wide and 1.2 times as wide as eye height and 0.56 times as wide as head; densely punctate; clypeus sparsely punctate, almost straight apically, not sharply pointed medially. Tentorial index 0.39. Malar space 0.64 times basal width of mandible. Antenna 27-28-segmented; F1 0.94 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.3, 3.6 and 1.4 times their width, respectively.

Mesosoma: 1.5 times as long as high. Pronotal trough crenulate anteriorly, collar rugulose-reticulate, rest of pronotal side largely smooth. Notauli deep and crenulate; mesonotum densely punctulate. Subalar fossa largely smooth with some punctures; precoxal sulcus glabrate; disc of mesopleuron puncticulate. Metapleuron largely puncticulate, rugulose-rugose ventrally. Propodeum punctulate anteriorly, rather rugose-reticulate posteriorly; with median longitudinal carina anteriorly and transverse carina; with narrow medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 2.8 times as long as wide; 1/R1 almost as long as stigmal length; basal posterior section of stigma 1.1 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 8.1: 2.6; m-cu: 2/Rs+M=1.9: 1; 1cu-a postfurcal, 1/Cu: 2/Cu=0.10: 1. Hindwing: r-m: 1/M=0.47: 1; 1/M: Cu&cu-a=2.3: 1.

Hind leg: Coxa with rugulae dorsobasally. Lengths of femur, tibia and basitarsus 4.6, 8.0 and 5.0 times their width, respectively; tibia 1.3 times as long as femur; inner and outer spurs of tibia 0.48 and 0.40 times as long as basitarsus, respectively.

Metasoma: 1.6 times as long as wide; apically not incurved. T1 0.73 times as long as wide apically, costate, basally rather smooth between dorsal carinae; dorsal carinae distinct basally; T2+T3 1.0 times as long as wide. T2 costate; T3 smooth. Apical rim of carapace moderately emarginated. Ovipositor sheath 0.19 times as long as forewing.

Color: Black; palpi and tegula yellow. Antenna blackish brown. Wings hyaline, stigma dark brown, veins yellow. Legs yellow, telotarsi, hing tibia about apical half and tarsus dark brown. Ovipositor sheath dark brown.

Lengths: Body 2.9 mm, antenna 2.7 mm, forewing 3.1 mm, ovipositor sheath 0.58 mm.

Male: Unknown.

Holotype: ♀, Tsuifeng, XI.1985 (KSL). Paratype: Meifeng, 1♀, VIII.1984 (KSL & KCC).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species differs from the other Taiwanese *Triaspis* species by the precox-

al sulcus and metasomal tergum III smooth.

Etymology: *Calvus* means smooth in Latin, refers to T3 smooth.

Triaspis (*Schizoprymnus*) *chiu* sp. n.

(Figs. 42, 67, 93, 121, 145, 168, 192, 221, 249)

Female: Head: 1.9 times as wide as long and 1.2 times wider than mesonotum. Eye 1.2 times as long as temple. Temple, frons (except glabrous medially) and vertex punctulate; without large lamellate frontal carina. POL: OD: OOL=1: 0.62: 1.4. Face 0.58 times as high as wide and 1.2 times as wide as eye height and 0.58 times as wide as head; punctulate; clypeus puncticulate, concave apically, sharply pointed medially. Tentorial index 0.64. Malar space 1.0 times basal width of mandible. Antenna 19-segmented; F1 1.0 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.3, 3.3 and 1.3 times their width, respectively.

Mesosoma: 1.3 times as long as high. Pronotal side rugose-punctate posteriorly; collar rugulose-rugose ventrally; rest largely smooth. Notauli deep and crenulate; mesoscutum punctulate, middle lobe rugose-reticulate posteriorly, sculptures on lateral lobe sparser; scutellum puncticulate. Subalar fossa punctate with carina; precoxal sulcus rugose-punctate; disc of mesopleuron puncticulate. Metapleuron rather rugulose - reticulate. Propodeum rugose-reticulate; with median longitudinal carina anteriorly and short transverse carina, they meet to form sharp projection; without medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 2.5 times as long as wide; 1/R1 shorter than stigmal length; basal posterior section of stigma 1.0 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 8.0: 2.6; m-cu: 2/Rs+M=1.8: 1; lcu-a postfurcal, 1/Cu: 2/Cu=0.20: 1. Hindwing: r-m: 1/M=0.67: 1; 1/M: Cu&cu-a=1.5: 1.

Hind leg: Coxa smooth. Lengths of femur, tibia and basitarsus 3.6, 7.7 and 3.7 times their width, respectively; tibia 1.3 times as long as femur; inner and outer spurs of tibia 0.62 and 0.54 times as long as basitarsus, respectively.

Metasoma: 1.3 times as long as wide, costate-rugose, interspace strigate; apically not incurved. T1 0.48 times as long as wide apically, basally rather smooth between dorsal carinae; dorsal carinae distinct basally; T2+T3 0.83 times as long as wide. Apical rim of carapace semicircularly emarginated. Ovipositor sheath 0.49 times as long as forewing.

Color: Blackish brown; palpi yellow, tegula dark brown. Antenna dark brown, lighter basally. Wings hyaline, stigma dark brown, veins yellow. Legs brownish yellow, hind tibia and tarsus darker. Ovipositor sheath dark brown.

Lengths: Body 1.9 mm, antenna 1.6 mm, forewing 1.8 mm, ovipositor sheath 0.88 mm.

Male: Unknown.

Holotype: ♀, Tungpu, 25-29.IX.1980 (LYC & TL).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species is close to *T. hui* sp. n., but differs from it by the posterior

carapace do not distinctly higher than anterior part, metacoxa smooth basally, and the vein 1/R1 of forewing shorter than stigmal length.

Etymology: The specific name is the Chinese noun "chiu" (ball). It refers to the shape of metasoma.

Triaspis (*Schizoprymnus*) *chouwen* sp. n.

(Figs. 23, 43, 68, 94, 122, 146, 169, 193, 220, 250)

Female: Head: 1.8 times as wide as long and 1.1 times wider than mesonotum. Eye 1.7 times as long as temple. Temple punctulate; frons rugulose medially, punctulate laterally; without large lamellate frontal carina. POL: OD : OOL=1: 0.50: 1.1. Vertex punctulate, rugulose around anterior ocellus. Face 0.44 times as high as wide and 1.2 times as wide as eye height and 0.62 times as wide as head; densely punctate, rugulose dorsally; clypeus sparsely punctate, almost straight, not sharply pointed medially. Tentorial index 0.61. Malar space 0.80 times basal width of mandible. Antenna 20-segmented; F1 0.92 times as long as F2; lengths of F1, F2 and penultimate flagellomere 2.7, 2.7 and 1.1 times their width, respectively.

Mesosoma: 1.4 times as long as high. Pronotal side smooth dorsally; medially crenulate; posteriorly and ventrally rather rugulose. Notauli deep and crenulate; mesoscutum densely punctate, middle lobe rugulose posteriorly, punctures on lateral lobe sparser; scutellum puncticulate. Subalar fossa and precoxal sulcus rugose-reticulate; disc of mesopleuron rugose-reticulate dorsally, puncticulate ventrally. Metapleuron rugose-reticulate. Propodeum rugose-reticulate; with median longitudinal carina anteriorly and short transverse carina, without medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 2.8 times as long as wide; 1/R1 longer than stigmal length; basal posterior section of stigma 1.2 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 6.9: 2.2; m-cu: 2/Rs+M=1.9: 1; lcu-a postfurcal, 1/Cu: 2/Cu=0.20: 1. Hindwing: r-m: 1/M=0.65: 1; 1/M: Cu&cu-a=1.3: 1.

Hind leg: Coxa rugose dorsobasally. Lengths of femur, tibia and basitarsus 3.8, 8.0 and 4.5 times their width, respectively; tibia 1.3 times as long as femur; inner and outer spurs of tibia 0.56 and 0.50 times as long as basitarsus, respectively.

Metasoma: 1.3 times as long as wide; rugose-reticulate; apically not incurved. T1 0.50 times as long as wide apically; dorsal carinae disinct in basal 0.4; T2+T3 0.83 times as long as wide. Apical rim of carapace deeply emarginated; rim of carapace behind weakly denticulate. Ovipositor sheath 0.58 times as long as forewing.

Color: Black; palpi yellow, tegula dark brown. Antenna dark brown, basally yellowish brown. Wings hyaline, stigma dark brown, veins yellow. Legs yellowish brown. Ovipositor sheath dark brown.

Lengths: Body 2.5 mm, antenna 1.8 mm, forewing 2.5 mm, ovipositor sheath 1.4 mm.

Male: Unknown.

Holotype: ♀, Kukuan, 14-17.X.1980 (KSL & CHW).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species differs from other Taiwanese *Triaspis* by the rim of carapace behind weakly denticulate.

Etymology: The specific is the Chinese noun "chouwen" (wrinkle). It refers to the propodeum rugose-reticulate.

Triaspis (*Schizoprymnus*) *chunji* sp. n.

(Figs. 30, 44, 69, 95, 123, 147, 170, 204, 230, 251)

Female: Head: 1.7 times as wide as long and 1.1 times wider than mesonotum. Eye 1.1 times as long as temple. Temple, frons and vertex punctulate; frons largely glabrate medially, with carinae near toruli; without large lamellate frontal carina. POL: OD: OOL =1: 0.75: 2.0. Face 0.53 times as high as wide and 1.1 times as wide as eye height and 0.57 times as wide as head; densely punctate; clypeus punctate dorsally, rugose ventrally, almost straight apically, not sharply pointed medially. Tentorial index 0.75. Malar space 0.86 times basal width of mandible. Antenna 21-22-segmented; F1 0.89 times as long as F2; lengths of F1, F2 and penultimate flagellomere 2.4, 2.7 and 1.0 times their width, respectively.

Mesosoma: 1.3 times as long as high. Pronotal side medially crenulate-punctate; posteriorly foveate; anteroventrally rugose-punctate; rest smooth. Notauli deep and crenulate; mesoscutum punctulate, middle lobe rugose-reticulate posteriorly; scutellum puncticulate. Subalar fossa and precoxal sulcus rugose-reticulate; disc of mesopleuron puncticulate. Metapleuron largely rugose-reticulate, rather smooth dorsally. Propodeum rugose-reticulate, anteriorly rather smooth; with median longitudinal carina anteriorly and transverse carina, with wide medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 2.6 times as long as wide; 1/R1 longer than stigmal length; basal posterior section of stigma 1.2 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 9.3: 3.0; m-cu: 2/Rs+M=1.5: 1; lcu-a postfurcal, 1/Cu: 2/Cu=0.18: 1. Hindwing: r-m: 1/M=0.67: 1; 1/M: Cu&cu-a=1.9: 1.

Hind leg: Coxa rugose dorsobasally. Lengths of femur, tibia and basitarsus 3.7, 7.5 and 6.0 times their width, respectively; tibia 1.3 times as long as femur; inner and outer spurs of tibia 0.43 and 0.40 times as long as basitarsus, respectively.

Metasoma: 1.6 times as long as wide; costate-rugose; apically not incurved. T1 0.56 times as long as wide apically; basally rugose-reticulate between dorsal carinae; dorsal carinae distinct anteriorly; T2+T3 1.1 times as long as wide. Apical rim of carapace strongly emarginated. Ovipositor sheath 0.27 times as long as forewing.

Color: Black; palpi yellow, tegula dark brown. Antenna blackish brown. Wings hyaline, stigma and veins dark brown. Legs brownish yellow; hind tibia apically and tarsus dark brown. Ovipositor sheath blackish brown.

Lengths: Body 3.5 mm, antenna 4.9 mm, forewing 3.6 mm, ovipositor sheath 0.98 mm.

Male: Unknown.

Holotype: ♀, Meifeng, V.1984 (KSL & KCC). Paratypes: Meifeng, 1♀, 24-26.VI.1981 (KSL & WST); 1♀, VIII.1984 (KSL & KCC). Tsuifeng, 1♀, VI.1984 (KSL & KCC).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species is close to *T. curvatus* sp. n., but differs from it by the clypeus distinctly rugose ventrally and almost straight apically, and the precoxal sulcus rugose-reticulate.

Etymology: The specific name is the Chinese noun "chunji" (clypeus). It refers to the clypeus punctate dorsally, rugose ventrally.

Triaspis (*Schizoprymnus*) *curvatus* sp. n.

(Figs. 32, 45, 70, 96, 124, 148, 186, 212, 236, 252)

Female: Head: 1.7 times as wide as long and 1.2 times wider than mesonotum. Eye 1.9 times as long as temple. Temple, frons and vertex punctulate; frons largely glabrate medially, with some carinae medioventrally; without large lamellate frontal carina. POL: OD: OOL=1: 0.71: 1.5. Face 0.53 times as high as wide and 1.2 times as wide as eye height and 0.59 times as wide as head; densely punctate; clypeus densely punctate dorsally, sparsely punctate ventrally, concave apically, not sharply pointed medially. Tentorial index 0.85. Malar space 0.75 times basal width of mandible. Antenna 23-25-segmented; F1 0.94 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.2, 3.4 and 1.0 times their width, respectively.

Mesosoma: 1.4 times as long as high. Pronotal side largely foveate-reticulate, smooth dorsally, Notauli deep and crenulate; mesoscutum punctulate, scutellum puncticulate. Subalar fossa and precoxal sulcus foveate; disc of mesopleuron foveate dorsally, rest puncticulate. Metapleuron rugose-reticulate. Propodeum rugose-reticulate; with median longitudinal carina anteriorly and short transverse carina, without medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 2.7 times as long as wide; 1/R1 longer than stigmal length; basal posterior section of stigma 1.2 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 8.1: 2.5; m-cu: 2/Rs+M=2.0: 1; lcu-a postfurcal, 1/Cu: 2/Cu=0.25: 1. Hindwing: r-m: 1/M=0.74: 1; 1/M: Cu&cu-a=1.6: 1.

Hind leg: Coxa smooth. Lengths of femur, tibia and basitarsus 3.8, 7.6 and 5.6 times their width, respectively; tibia 1.4 times as long as femur; inner and outer spurs of tibia 0.43 and 0.36 times as long as basitarsus, respectively.

Metasoma: 1.6 times as long as wide; costate-rugose, interspace strigate; apicoventrally slightly incurved. T1 0.54 times as long as wide apically, basally rugose-reticulate between dorsal carinae; dorsal carinae distinct anteriorly; T2+T3 1.1 times as long as wide. Apical rim of carapace moderately emarginated. Ovipositor sheath 0.39 times as long as forewing.

Color: Blackish brown; palpi yellow, tegula dark brown. Antenna dark brown, basally brownish yellow. Wings hyaline, stigma and veins dark brown. Legs brownish yellow; hind tibia (except base) dark brown. Ovipositor sheath dark brown.

Lengths: Body 2.7 mm, antenna 2.3 mm, forewing 2.6 mm, ovipositor sheath 1.0 mm.

Male: Unknown.

Holotype: ♀, Lienhuachih, V.1984 (KSL & KCC). Paratypes: Lienhuachih, 1♀, IV, & 4♀, V.1984 (KSL & KCC). Wanfeng, 2♀, IV.1984 (KSL & KCC).

Distribution: Taiwan.

Host: Unknown.

Remarks: The species is close to *T. chunji* sp. n., but differs from it by the clypeus sparsely punctate ventrally and cuncave apically, and the precoxal sulcus foveate.

Etymology: *Curvatus* means curved in Latin, refers to its clypeus concave medially.

Triaspis (*Schizoprymnus*) *distinctus* sp. n.

(Figs. 19, 46, 71, 97, 125, 149, 171, 197, 228, 253)

Female: Head: 1.7 times as wide as long and 1.3 times wider than mesonotum. Eye 1.2 times as long as temple. Temple, frons (medially glabrous) and vertex puncticulate; without large lanellate frontal carina. POL: OD: OOL=1: 0.60: 1.5. Face 0.55 times as high as wide and 1.2 times as wide as eye height and 0.60 times as wide as head, densely punctate; clypeus puncticulate dorsally, densely punctate ventrally, almost straight apically, not sharply pointed medially. Tentorial index 0.54. Malar space 0.67 times basal width of mandible. Antenna 23-25-segmented; F1 0.93 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.5, 3.8 and 1.3 times their width, respectively.

Mesosoma: 1.4 times as long as high. Pronotal side largely smooth, pronotal trough crenulate anteriorly, collar rugulose anteriorly. Notauli deep and crenulate; mesoscutum punctulate, scutellum puncticulate. Subalar fossa punctate with carinae; precoxal sulcus strigate; disc of mesopleuron puncticulate. Metapleuron smooth dordally, rugulose-rugose ventrally. Propodeum smooth anteriorly, posteriorly smooth to foveate with rugae; with median longitudinal carina and transverse carina, with wide medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 2.6 times as long as wide; 1/R1 almost as long as stigmal length; basal posterior section of stigma 1.1 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 7.4: 2.1; m-cu: 2/Rs+M=1.6: 1; lcu-a postfurcal, 1/Cu: 2/Cu=0.20: 1. Hindwing: r-m: 1/M=0.43: 1; 1/M: Cu&cu-a=2.3: 1.

Hind leg: Coxa smooth. Lengths of femur, tibia and basitarsus 4.5, 7.3 and 6.7 times their width, respectively; tibia 1.3 times as long as femur; inner and outer spurs of tibia 0.45 and 0.40 times as long as basitarsus, respectively.

Metasoma: 1.5 times as long as wide; rugose-costate; apically not incurved. T1 0.57 times as long as wide apically; basally rugose-reticulate between dorsal carinae; dorsal carinae disinct anteriorly; T2+T3 1.1 times as long as wide; T3 smooth apically. Apical rim of carapace moderately emarginated. Ovipositor sheath 0.33 times as long as forewing.

Color: Blackish brown; palpi and tegula brownish yellow. Antenna dark brown, basally lighter. Wings hyaline, stigma and veins brown. Legs brownish yellow; hind tibia (except base) dark brown. Ovipositor sheath dark brown.

Lengths: Body 2.4 mm, antenna 2.2 mm, forewing 2.4 mm, ovipositor sheath 0.78 mm.

Male: Similar to female.

Holotype: ♀, Tsuifeng, 12-14.IX.1984 (KSL & SCL). Paratypes: Hoshe, 1 ♀, 22.VII. 1982 (LYC & KCC). Meifeng, 1♀, 4-7.X.1982 (KCC); 1♀, V, & 1♀, VI.1984 (KSL & KCC). Tayuling, 1♀, 12-15.IX.1980 (KSL & CHW); 3♀, 6-9.IX.1983 (LYC & KCC). Tsuifeng, 22♀, 1-3.VIII.1981 (TL & WST); 24♀, 1-3.IX.1982 (LYC & KCC); 2♀, 23-25.VI.1983 (KSL & SCL); 8♀, 5.VIII.1984 (KSL); 3♀, 15-16.VIII.1984 (KCC); 38♀, 12-14.IX.1984 (KSL & SCL). Tungpu, 1♀, 25-29.IX.1980 (LYC & TL); 1♀, 5-6.X.1981 (TL & WST); 1♀, 18-21.X.1982 (KCC & SCL); 1♀, 13-16.XII.1982 (KCC & CCP); 1♀, 20-24.VI.1983 (KCC & CYW); 6 ♀, X.1985 (KSL); 2♀, XI.1985 (KSL). Wuling, 2♀, 27-29.VI.1979 (KSL & LYC).Wushe, 6♀1 ♂, V.1983 (HT)(in AEI).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species is close to *Schizoprymnus ungularis* Belokobylskij, 1994, but differs from it by the temple in dorsal view rather constricted, and the anterior shape of carapace in dorsal view.

Triaspis (*Schizoprymnus*) *fessus* sp. n.

(Figs. 24, 47, 72, 98, 126, 150, 176, 203, 231, 254)

Female: Head: 1.6 times as wide as long and 1.1 times wider than mesonotum. Eye 1.2 times as long as temple. Temple, frons (medially glabrous) and vertex puncticulate; without large lamellate frontal carina. POL: OD: OOL=1: 0.83: 2.1. Face 0.59 times as high as wide and 1.0 times as wide as eye height and 0.57 times as wide as head; punctulate; clypeus rugulose-punctate, weakly convex apically, not sharply pointed medially. Tentorial index 0.64. Malar space 0.75 times basal width of mandible. Antenna 24-segmented; F1 0.88 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.5, 4.0 and 1.3 times their width, respectively.

Mesosoma: 1.5 times as long as high. Pronotal side rugulose dorsoposteriory, pronotal trough crenulate; collar rugulose-reticulate anteriorly, rest of pronotal side largely smooth. Notauli deep and crenulate; mesoscutum punctulate, middle lobe reticulate-rugose posteriorly; scutellum puncticulate. Subalar fossa foveate with rugae; precoxal sulcus crenulate; disc of mesopleuron puncticulate. Metapleuron punctulate dorsally, rugose-reticulate ventrally. Propodeum rugose-reticulate; with median longitudinal carina anteriorly, transverse carina and medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 2.6 times as long as wide; 1/R1 longer than stigmal length; basal posterior section of stigma; 1.1 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 10.0: 2.9; m-cu: 2/Rs+M=1.8: 1; 1cu-a postfurcal, 1/Cu: 2/Cu=0.22: 1. Hindwing: r-m: 1/M=0.43: 1; 1/M: Cu&cu-a=1.9: 1.

Hind leg: Coxa rugulose dorsobasally. Lengths of femur, tibia and basitarsus 4.0, 8.9

and 6.7 times their width, respectively; tibia 1.3 times as long as femur; inner and outer spurs of tibia 0.48 and 0.38 times as long as basitarsus, respectively.

Metasoma: 1.6 times as long as wide; costate-rugose, interspace strigulate; apically not incurved. T1 0.72 times as long as wide apically; basally rugulose between dorsal carina; dorsal carinae distinct anteriorly; T2+T3 1.0 times as long as wide. Apical rim of carapace weakly emarginated. Ovipositor sheath 0.28 times as long as forewing.

Color: Dark brown; palpi yellow. Antenna dark brown, basal segments lighter. Wings hyaline, stigma dark brown, veins yellow. Legs brownish yellow; hind tibia posteriorly and tarsus more or less darker. Ovipositor sheath blackish brown.

Lengths: Body 2.5 mm, antenna 2.3 mm, forewing 2.5 mm, ovipositor sheath 0.70 mm.

Male: Unknown.

Holotype: ♀, Tungpu, 23-27.VII.1984 (KCC & CHY).

Distribution: Tawian.

Host: Unknown.

Remarks: This species differs from the other Taiwanese *Triaspis* species by the following combination of characters: vein 1/R1 of forewing distinctly longer that stigmal length; metasoma in dorsal view constricted posteriorly; ovipositor sheath distinctly shorter than carapace.

Etymology: *Fessus* means feeble in Latin, refers to its vein 3+4/Rs of forewing weakly curved.

Triaspis (*Schizoprymnus*) *hui* sp. n.

(Figs. 15, 48, 73, 99, 127, 151, 172, 194, 222, 255)

Female: Head: 1.9 times as wide as long and 0.97 times wider than mesonotum. Eye 1.2 times as long as temple. Temple and vertex puncticulate; frons punctulate laterally, strigate medioventrally, smooth mediodorsally; without large lamellate frontal carina. POL: OD: OOL=1 : 0.61 : 1.4. Face 0.53 times as high as wide and 1.2 times as wide as eye height and 0.59 times as wide as head; densely punctate, with some rugosity mediodorsally, clypeus densely punctate, concave apically, with sharply pointed medially. Tentorial index 0.73. Malar space 0.91 times basal width of mandible. Antenna 23-segmented; F1 0.82 times as long as F2; lengths of F1, F2 and penultimate flagellomere 2.8, 3.4 and 1.5 times their width, respectively.

Mesosoma: 1.3 times as long as high. Pronotal side crenulate medially, rugose-reticulate dorsoposteriorly, collar largely rugulose-punctate, rest of pronotal side smooth. Notauli deep and crenulate, mesoscutum punctulate, middle lobe rugose-reticulate posteriorly, scutellum puncticulate. Subalar fossa foveate with carinae; precoxal sulcus rugose-reticulate; disc of mesopleuron sparsely punctate. Metapleuron rugose-reticulate. Propodeum rugose-reticulate; with median longitudinal carina and short transverse carina, they meet to form sharp projection; without distinct medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 2.5 times as long as wide; 1/R1 almost as long as stigmal

length; basal posterior section of stigma 1.2 temes apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1 : 7.6 : 2.2; m-cu: 2/Rs+M=1.2: 1; 1cu-a postfurcal, 1/Cu: 2/Cu=0.27: 1. Hindwing: r-m: 1/M=0.56: 1; 1/M: Cu&cu-a=1.9: 1.

Hind leg: Coxa rugulose dorsobasally. Lengths of femur, tibia and basitarsus 3.8, 7.6 and 4.4 times their width, respectively, tibia 1.3 times as long as femur; inner and outer spurs of tibia 0.55 and 0.50 times as long as basitarsus, respectively.

Metasoma: 1.3 times as long as wide, rugose-reticulate; apically not incurved. T1 0.58 times as long as wide apically; dorsal carinae distinct basally, T2+T3 0.92 times as long as wide. Apical rim of carapace strongly emarginated. Ovipositor sheath 0.41 times as long as forewing.

Color: Black; palpi yellow, tegula dark brown. Antenna blackish brown, basally brown. Wings hyaline, stigma and veins dark brown. Legs yellowish brown, telotarsi, hind tibia apically and tarsus dark brown. Ovipositor sheath dark brown.

Lengths: Body 2.6 mm, antenna 2.1 mm, forewing 2.9 mm, ovipositor sheath 1.2 mm.

Male: Unknown.

Holotype: ♀, Lushan, 27-31.V.1980 (KSL & LYC). Paratype: 1♀, same date as holotype.

Distribution: Taiwan.

Host: Unknown.

Remarks: This species is close to *T. chiu* sp. n., but differs from it by the posterior carapace is distinctly higher than anterior part, metacoxa rugulose basally, and the vein 1/R1 of forewing almost as long as stigmal length.

Etymology: The specific name is the Chinese noun "hui" (beak). It refers to the projection of propodeum.

Triaspis (*Schizoprymnus*) *imitatus* Papp

(Figs. 14, 41, 66, 92, 120, 144, 182, 207, 224, 248)

Schizoprymmus (*Schizoprymmnus*) *imitatus* Papp, 1993. Acta Zool. Hung. 39 : 145.

Female: Head: 1.7 times as wide as long and 1.4 times wider than mesonotum. Eye 1.4 times as long as temple. Temple, frons and vertex rather densely punctulate; without large lamellate frontal carina. POL: OD: OOL=1 : 0.60 : 1.7. Face 0.48 times as high as wide and 1.4 times as wide as eye height and 0.59 times as wide as head, densely punctate; clypeus densely punctate, almost straight to weakly concave apically, with or without faintly pointed medially. Tentorial index 1.2. Malar space 0.94 times basal width of mandible. Antenna 25-27-segmented; F1 0.95 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.3, 3.2 and 1.3 times their width, respectively.

Mesosoma: 1.5 times as long as high. Pronotal side foveate-reticulate medially and dorsoposteriorly, collar largely rugose-reticulate to rugulose-punctate, rest of pronotal side smooth. Notauli deep and crenulate; mesonotum punctulate, middle of mesoscutum foveate. Subalar fossa and precoxal sulcus foveate; disc of mesopleuron sparsely punctate.

Metapleuron rugose-reticulate. Propodeum rugose-reticulate; with median longitudinal carina and transverse carina, without medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 3.1 times as long as wide; 1/R1 almost as long as stigmal length; basal posterior section of stigma 1.5 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1 : 7.6 : 3.0; m-cu: 2/Rs+M=2.3: 1; lcu-a postfurcal, 1/Cu: 2/Cu=0.16: 1. Hindwing: r-m: 1/M=0.45: 1; 1/M: Cu&cu-a=1.8: 1.

Hind leg: Coxa smooth. Lengths of femur, tibia and basitarsus 4.4, 9.5 and 6.3 times their width, respectively; tibia 1.5 times as long as femur; inner and outer spurs of tibia 0.37 and 0.32 times as long as basitarsus, respectively.

Metasoma: 2.1 times as long as wide, rugose-reticulate; apicoventrally distinctly incurved. T1 0.80 times as long as wide apically; dorsal carinae distinct basally; T2+T3 1.3 times as long as wide. Apical rim of carapace semicircularly emarginated. Ovipositor sheath 0.19 times as long as forewing.

Color: Black; palpi yellow, tegula brownish yellow. Antenna dark brown, scape and pedicel lighter. Wings hyaline, stigma dark brown, veins brownish yellow. Legs yellow, hind tibia apically and tarsus largely dark brown. Ovipositor sheath dark brown.

Lengths: Body 3.8 mm, antenna 3.1 mm, forewing 3.5 mm, ovipositor sheath 0.68 mm.

Male: Similar to female. Antenna longer and slender.

Specimens examned: Lienhuachih, 1♀, V, 4♀, VIII, & 19♀, IX.1984 (KSL & KCC). Lushan, 1♀, 27-31.V.1980 (KSL & LYC). Wushe, 1♀1♂, 29.V.1983 (HT)(in AEI).

Distribution: Taiwan.

Host: Unknown.

Triaspis (Schizoprymnus) ketiao sp. n.

(Figs. 25, 49, 74, 100, 128, 152, 177, 205, 233, 256)

Female: Head: 1.6 times as wide as long and 1.1 times wider than mesonotum. Eye 1.1 times as long as temple. Temple, frons and vertex punctulate; without large lamellate frontal carina. POL: OD: OOL=1 : 0.83 : 2.0. Face 0.62 times as high as wide and 1.0 times as wide as eye height and 0.55 times as wide as head; densely punctate, with rugae near toruli, clypeus punctulate, almost straight apically, not sharply pointed medially. Tentorial index 0.58. Malar space 1.0 times basal width of mandible. Antenna 16-18-segmented; F1 1.0 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.4, 3.3 and 1.0 times their width, respectively.

Mesonoma: 1.4 times as long as high. Pronotal side rather densely punctulate dorsally, medially and dorsoposteriorly rugulose-punctate; collar rugulose ventrally, rest of pronotal side smooth. Notauli deep and crenulate; mesoscutum punctulate; scutellum puncticulate. Subalar fossa more or less foveolate, with carinae; precoxal sulcus crenulate; disc of mesopleuron puncticulate. Metapleuron smooth dorsally, rugose-reticulate ventrally. Propodeum rugose-reticulate; with median longitudinal carina anteriorly and short transverse carina, they meet to form weak projection; with ill defined medioposterior area; lateral

propodeal tubercles distinct.

Wings: Forewing: stigma 2.6 times as long as wide, 1/R1 almost as long as stigmal length; basal posterior section of stigma 1.2 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1 : 8.3: 2.3; m-cu: 2/Rs+M=1.6: 1; 1 cu-a postfurcal, 1/Cu: 2/Cu=0.14: 1. Hindwing: r-m: 1/M=0.38: 1; 1/M: Cu&cu-a=2.2: 1.

Hind leg: Coxa with rugulae dorsobasally. Lengths of femur, tibia and basitaarsus 3.7, 7.5 and 5.0 times their width, respectively; tibia 1.4 times as long as femur; inner and outer spurs of tibia 0.45 and 0.35 times as long as basitarsus, respectively,

Metasoma: 1.7 times as long as wide, costate; apically not incurved. T1 0.68 times as long as wide apically, basally rather smooth between dorsal carinae; dorsal carinae distinct anteriorly; T2+T3 1.1 times as long as wide; T3 smooth apically. Apical rim of carapace strongly emarginated. Ovipositor sheath 0.37 times as long as forewing.

Color: Black; palpi brownish yellow, tegula dark brown. Antenna blackish brown, scape and pedicel lighter. Wings hyaline, stigma dark brown, veins yellowish brown. Legs brownish yellow, telotarsi, hind tibia (except base) and tarsus darker. Ovipositor sheath blackish brown.

Lengths: Body 2.4 mm, antenna 1.6 mm, forewing 2.4 mm, ovipositor sheath 0.88 mm.

Male: Unknown.

Holotype: ♀, Meifeng, XI.1985 (KSL). Paratypes: Alishan, 1♀, 17-20.VIII.1982 (KCC & CCP). Meifeng, 1♀, 2-4.VI.1980 (LYC & CCC); 1♀, 22-26.VI.1983 (KSL & SCL); 1♀, 8-11. V.1984 (KCC & CCP); 1♀, IX.1984 (KSL & KCC); 1♀, XI.1985 (KSL). Sungkang, 1♀, X. 1984 (KSL & KCC); 1♀, XI.1985 (KSL). Tsuifeng, 2♀, X.1984 (KSL & KCC).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species differs from the other Taiwanese *Triaspis* species by the following combination of characters: vein 1/R1 of forewing almost as long as stigmal length, carinae on T1+T2 more straight and parallel; antenna 16-18-segmented; and metasoma 1.7 times as long as wide.

Etymology: The specific name is the Chinese noun "ketiao" (costate). It refers to the sculptures of carapace.

Triaspis (Schizoprymnus) kueichia sp. n.

(Figs. 20, 50, 75, 101, 129, 153, 173, 199, 234, 257)

Female: Head: 1.8 times as wide as long and 1.1 times wider than mesonotum. Eye 1.3 times as long as temple. Temple punctulate; frons rather densely punctulate, punctate-rugose medially; without large lamellate frontal carina. POL: OD: OOL=1 : 0.63 : 1.6. Face 0.57 times as high as wide and 1.1 times as wide as eye height and 0.58 times as wide as head; densely punctate, with rugae near toruli; clypeus punctate, almost straight apically, not sharply pointed medially. Tentorial index 0.53. Malar space 0.80 times basal width of mandible. Antenna 23-25-segmented; F1 0.94 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.0, 3.2 and 1.3 times their width, respectively.

Mesosoma: 1.3 times as long as high. Pronotal trough crenulate, collar more or less rugulose-reticulate, rest of pronotal side largely smooth. Notauli deep and crenulate; mesoscutum punctulate, scutellum puncticulate. Subalar fossa largely smooth, with carinae; precoxal sulcus rugulose-punctate; disc of mesopleuron puncticulate. Metapleuron puncticulate dorsally, rugose-reticulate ventrally. Propodeum punctulate anteriorly, posteriorly smooth, and densely punctate along carinae; with median longitudinal carina anteriorly and short transverse carina, with ill defined medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing stigma 2.4 times as long as wide; 1/R1 longer than stigmal length; basal posterior section of stigma 1.1 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1 : 7.1 : 2.0; m-cu: 2/Rs+M=1.4: 1 ; 1cu-a postfurcal, 1/Cu: 2/Cu=0.14: 1. Hindwing: r-m: 1/M=0.58: 1; 1/M : Cu&cu-a=1.6: 1.

Hind leg: Coxa rugose dorsobasally. Lengths of femur, tibia and basitarsus 3.4, 6.9 and 5.6 times their width, respectively; tibia 1.3 times as long as femur; inner and outer spurs of tibia 0.36 and 0.32 times as long as basitarsus, respectively.

Metasoma: 1.2 times as long as wide; costate-rugose, interspace strigulate to strigate; apically not incurved. T1 0.55 times as long as wide apically; basally rather smooth between dorsal carinae; dorsal carinae distinct anteriorly; T2+T3 0.76 times as long as wide. Apical rim of carapace moderately emarginated. Ovipositor sheath 0.55 times as long as forewing.

Color: Black; palpi yellowish brown; tegula blackish brown. Antenna blackish brown. Wings hyaline, stigma and veins dark brown. Legs yellowish brown; hind tibia and tarsus dark brown. Ovipositor sheath blackish brown.

Lengths: Body 2.5 mm, antenna 2.5 mm, forewing 3.0 mm, ovipositor sheath 1.7 mm.

Male: Unknown.

Holotype: ♀, Meifeng, 5-9.X.1980 (CCC & CCCh). Paratypes: Meifeng, 1♀, same data as holotype. Sungkang, 1♀, X.1984 (KSL & KCC).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species is close to *T. ovatus* sp. n., but differs from it by the ovipositor sheath 0.55 times as long as forewing length; the metasoma 1.2 times as long as wide and the antenna 17-20-segmented.

Etymology: The specific name is the Chinese noun "kueichia" (carapace). It refers to the shape of metasoma.

Triaspis (*Schizoprymnus*) *lienhuachihensis* sp. n.

(Figs. 26, 51, 76, 102, 130, 154, 183, 209, 218, 258)

Female: Head: 1.6 times as wide as long and 1.3 times wider than mesonotum. Eye 1.3 times as long as temple. Temple, frons and vertex punctulate; frons with some rugae near toruli, with large lamellate frontal carina. POL: OD: OOL=1 : 0.63 : 1.6. Face 0.45 times as high as wide and 1.2 times as wide as eye height and 0.59 times as wide as head; densely punctate, with some rugae dorsally; clypeus densely punctate, almost straight apically, not

sharply pointed medially. Tentorial index 0.75. Malar space 0.67 times basal width of mandible. Antenna 26-segmented; F1 1.0 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.5, 3.1 and 1.1 times their width, respectively.

Mesosoma: 1.5 times as long as high. Pronotal side punctulate dorsally, medially and posteriorly foveate, collar rugulose-punctate. Notauli deep and crenulate; mesonotum punctulate, middle lobe of mesoscutum foveolate posteriorly. Subalar fossa and precoxal sulcus foveate; disc of mesopleuron sparsely punctate. Metapleuron rugose-reticulate. Propodeum rugose-reticulate; with median longitudinal carina anteriorly and transverse carina, without medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 2.8 times as long as wide; 1/R1 slightly shorter than stigmal length; basal posterior section of stigma 1.2 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1 : 7.0 : 2.5; m-cu : 2/Rs+M=2.3: 1; 1cu-a postfurcal, 1/Cu: 2/Cu=0.18: 1. Hindwing: r-m: 1/M=0.52: 1; 1/M: Cu&cu-a=1.9: 1.

Hind leg: Coxa rugose dorsobasally. Lengths of femur, tibia and basitarsus 4.2, 8.8 and 6.5 times their width, respectively; tibia 1.4 times as long as femur; inner and outer spurs of tibia 0.34 and 0.31 times as long as basitarsus, respectively.

Metasoma: 1.9 times as long as wide; rugose-reticulate; apicoventrally distinctly incurved. T1 0.69 times as long as wide apically; dorsal carinae distinct basally; T2+T3 1.3 times as long as wide. Apical rim of carapace weakly emarginated. Ovipositor sheath 0.25 times as long as forewing.

Color: Blackish brown; palpi brownish yellow, tegula yellowish brown. Antenna dark brown, basally lighter. Wings hyaline, stigma dark brown, veins yellow. Legs brownish yellow; hind tibia apically dark brown. Ovipositor sheath blackish brown.

Lengths: Body 2.7 mm, antenna 2.4 mm, forewing 2.5 mm, ovipositor sheath 0.63 mm.

Male: Unknown.

Holotype: ♀, Lienhuachih, V.1984 (KSL & KCC).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species is close to *T. borpian* sp, n., but differs from it by the frons punctulate laterally and the clypeus almost straight apically.

Etymology: The specific name is derived from the name of the type locality, Lienhuachih.

Triaspis (*Schizoprymnus*) *loi* sp. n.

(Figs. 27, 52, 77, 103, 131, 155, 184, 198, 225, 259)

Female: Head: 1.8 times as wide as long and 1.3 times wider than mesonotum, punctulate. Eye 1.2 times as long as temple. Frons rugulose-punctate medially, without large lamellate frontal carina. POL: OD: OOL=1 : 0.47 : 1.4. Face 0.41 times as high as wide and 1.5 times as wide as eye height and 0.66 times as wide as head; with some rugosity dorsomedially; clypeus almost straight apically, not sharply pointed medially. Tentorial index 1.2. Malar space 1.2 times basal width of mandible. Antenna 22-segmented; F1 0.93

times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.3, 3.1 and 1.3 times their width, respectively.

Mesosoma: 1.4 times as long as high. Pronotal side punctulate dorsally, rest rugose-reticulate. Notauli deep and crenulate; mesoscutum punctulate, middle lobe rugose-reticulate, scutellum puncticulate. Subalar fossa foveate; precoxal sulcus reticulate-rugose; disc of mesopleuron puncticulate. Metapleuron rugose-reticulate. Propodeum rugose-reticulate; with median longitudinal carina anteriorly and short transverse carina, without medioposterior area; lateral propodeal tubercles weakly developed.

Wings: Forewing: stigma 2.5 times as long as wide; 1/R1 almost as long as stigmal length; basal posterior section of stigma 1.3 times apical posterior section of stigma; r-rs: 3+4/Rs : 2/Rs=1 : 6.9 : 2.4; m-cu : 2/Rs+M=1.2: 1; lcu-a postfurcal, 1/Cu: 2/Cu=0.16: 1. Hindwing: r-m: 1/M=0.50: 1; 1/M : Cu&cu-a=2.0: 1.

Hind leg: Coxa rugose dorsobasally. Lengths of femur, tibia and basitarsus 4.0, 8.5 and 6.3 times their width, respectively; tibia 1.4 times as long as femur; inner and outer spurs of tibia 0.40 and 0.36 times as long as basitarsus, respectively.

Metasoma: 1.8 times as long as wide, rugose-reticulate; apicoventrally weakly incurved. T1 0.58 times as long as wide apically; dorsal carinae distinct basally; T2+T3 1.2 times as long as wide. Apical rim of carapace semicircularly emarginated. Ovipositor sheath 0.46 times as long as forewing.

Color: Black; palpi and tegula blackish brown. Antenna blackish brown, basally lighter. Wings hyaline, stigma dark brown, veins yellowish brown. Legs dark brown. Ovipositor sheath blackish brown.

Lengths: Body 2.5 mm, antenna 2.0 mm, forewing 2.3 mm, ovipositor sheath 1.0 mm.

Male: Unknown.

Holotype: ♀, Wuling, 27-29.VI.1979 (KSL & LYC). Paratypes: 1♀, same date as holotype.

Distribution: Taiwan.

Host: Unknown.

Remarks: This species differs from the other Taiwanese *Triaspis* species by the following combination of characters: vein 1/R1 of forewing almost as long as stigmal length, clylpeus not sharply pointed medially, tentorial index 1.2, and the metasoma elongate with apical rim semicircularly emarginate.

Etymology: Patronymic, named in honour of Mr. Kang-chen Lo.

Triaspis (Schizoprymnus) ovatus sp. n.

(Figs. 31, 53, 78, 104, 132, 156, 178, 211, 237, 260)

Female: Head: 1.7 times as wide as long and 1.1 times wider than mesonotum. Eye 1.2 times as long as temple. Temple, frons (glabrous medially) and vertex puncticulate; without large lamellate frontal carina. POL: OD: OOL=1 : 0.77 : 1.8. Face 0.66 times as high as wide and 1.0 times as wide as eye height and 0.53 times as wide as head; punctulate, with rugae near toruli; clypeus puncticulate, almost straight apically, not sharply pointed

medially. Tentorial index 0.69. Malar space 0.91 times basal width of mandible. Antenna 17-20-segmented; F1 0.94 times as long as F2; lengths of F1, F2 and penultimated flagellomere segment 3.2, 3.4 and 1.1 times their width, respectively.

Mesosoma: 1.4 times as long as high. Pronotal side more or less rugulose dorsoposteriorly, pronotal trough crenulate, collar rugose anteroventrally, rest of pronotal side largely smooth. Notauli deep and crenulate; mesonotum punctulate. Subalar fossa smooth to foveolate; precoxal sulcus strigate; disc of mesopleuron puncticulate. Metapleuron puncticulate dorsally, rugose-reticulate ventrally. Propodeum foveate with rugae, except basally punctate; with median longitudinal carina and strongly developed transverse carina; with ill defined medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 2.9 times as long as wide; 1/R1 longer than stigmal length; basal posterior section of stigma 1.0 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 7.3: 2.4; m-cu: 2/Rs+M=2.5: 1; 1cu-a postfurcal, 1/Cu: 2/Cu=0.19: 1. Hindwing: r-m: 1/M=0.41: 1; 1/M: Cu&cu-a=2.1: 1.

Hind leg: Coxa with rugae dorsobasally. Lengths of femur, tibia and basitarsus 3.5, 8.6 and 6.7 times their width, respectively; tibia 1.4 times as long as femur; inner and outer spurs of tibia 0.37 and 0.33 times as long as basitarsus, respectively.

Metasoma: 1.5 timesas long as wide, rugose-costate, interspace strigate; apically not incurved. T1 0.66 times as long as wide apically; dorsal carinae distinct anteriorly; T2+T3 0.97 times as long as wide. Apical rim of carapace moderately emarginated. Ovipositor sheath 0.69 times as long as forewing.

Color: Black; palpi yellow, tegula dark brown. Antenna blackish brown, scape brownish yellow. Wings hyaline, stigma and veins dark brown. Legs brownish yellow, hind tibia apically and tarsus brown. Ovipositor sheath dark brown.

Lengths: Body 3.1 mm, antenna 2.0 mm, forewing 3.4 mm, ovipositor sheath 2.3 mm.

Male: Unknown.

Holotype: ♀, Tsuifeng VIII.1984 (KSL & KCC). Paratypes: Meifeng, 1♀, 28-29.VIII. 1981 (LYC & SCL). 1♀, VIII.1984 (KSL & KCC). Sungakng, 1♀, 6.VIII.1984 (KSL), 1♀, X. 1984 (KSL & KCC). Tsuifeng, 4♀, VIII.1984 (KSL & KCC); 1♀, 5.VIII.1984 (KSL); 1♀, IX, & 3♀, X.1984 (KSL & KCC); & 2♀, IX, 1 ♀, X, & 1♀, XI.1985 (KSL). Tungpu, 1♀, 25-29.IX.1980 (LYC & TL); 1♀, XII.1985 (KSL).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species differs from the other Taiwanese *Triaspis* species by the following combination of characters: vein 1/R1 of forewing distinctly longer than stigmal length, ovipositor sheath 0.69 times as long as forewing length, metasoma 1.5 times as long as wide; antenna 17-20-segmented.

Etyology: *Ovatus* means egg-shaped in Latin, refers to its metasomal shape.

Triaspis (*Schizoprymnus*) *plenus* sp. n.

(Figs. 79, 105, 133 157, 185, 210, 238, 261)

Female: Head: 1.6 times as wide as long and 1.6 times wider than mesonotum. Eye 1.3 times as long as temple. Temple, frons and vertex puncticulate; without large lamellate frontal carina. POL: OD: OOL=1 : 0.60 : 1.8. Face 0.53 times as high as wide and 1.3 times as wide as eye height and 0.58 times as wide as head, punctulate; clypeus punctulate, almost straight apically, not sharply pointed medially. Tentorial index 1.0. Malar space 1.3 times basal width of mandible. Antenna 20-22-segmented; F1 1.0 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.7, 3.7 and 1.3 times their width, respectively.

Mesosoma: 1.6 times as long as high. Pronotal trough weakly crenulate, collar anteroventrally rugulose to rugulose-reticulate, rest of pronotal side largely smooth. Notauli deep and crenulate; mesonotum punctulate. Subalar fossa with carina; precoxal sulcus foveolate; disc of mesopleuron puncticulate. Metapleuron rugose-reticulate. Propodeum rugose-reticulate, rather smooth anteromedially; with median longitudinal carina and short transverse carina, without medioposterior area; lateral propodeal tubercles weakly developed.

Wings: Forewing: stigma 3.4 times as long as wide; 1/R1 shorter than stigmal length; basal posterior section of stigma 1.3 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 9.3: 2.7; m-cu: 2/Rs+M=1.5: 1; 1cu-a antefurcal. Hindwing: r-m: 1/M=0.43: 1; 1/M: Cu&cu-a=2.0: 1.

Hind leg: Coxa smooth. Lengths of femur, tibia and basitarsus 4.5, 10.0 and 7.0 times their width, respectively; tibia 1.4 times as long as femur; inner and outer spurs of tibia 0.23 and 0.19 times as long as basitarsus, respectively.

Metasoma: 1.9 times as long as wide, rugulose-costulate, rather smooth subspically; apicoventrally weakly incurved. T1 0.75 times as long as wide apically; dorsal carinae distinct basally; T2+T3 1.4 times as long as wide. Apical rim of carapace almost complete. Ovipositor sheath 0.27 times as long as forewing.

Color: Dark brown; palpi and tegula yellow. Antenna dark brown, basally lighter. Wings hyaline, stigma dark brown, veins yellow. Legs yellow, hind tibia apically and tarsus light brown. Ovipositor sheath dark brown.

Lengths: Body 2.0 mm, antenna 1.6 mm, forewing 1.8 mm, ovipositor sheath 0.48 mm.

Male: Unknown.

Holotype: ♀, Lienhuachih, IX.1984 (KSL & KCC). Paratype: Lanyu, 1♀, 4-9.V.1982 (KSL, KCC, SCL & CCP).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species differs from the other Taiwanese *Triaspis* species by the following combination of characters: vein 1/R1 of forewing shorter than stigmal length, clypeus not sharpy pointed medially, metasoma elongate with apical rim almost without emarginate, and the ovipositor sheath about 0.3 times as long as forewing.

Etymology: *Plenus* means full in Latin, refers to its carapace without distinct emargination.

Triaspis (Schizoprymnus) robustus sp. n.

(Figs. 21, 54, 80 106, 134, 158, 174, 200, 232, 262)

Female: Head: 1.7 times as wide as long and 1.1 times wider than mesonotum. Eye 1.0 times as long as temple. Temple and vertex puncticulate; frons punctulate laterally, strigate medioventrally, glabrous medioddorsally, without large lamellate frontal carina. POL: OD: OOL=1 : 0.50 : 1.4. Face 0.52 times as high as wide and 1.1 times as wide as eye height and 0.59 times as wide as head; punctulate, with rugae near toruli; clypeus puncticulate, almost straight apically, not sharply pointed medially. Tentorial index 0.50. Malar space 0.77 times basal width of mandible. Antenna 20-21-segmented; F1 1.1 times as long as F2; lengths of F1, F2 and penultimate flagellomere 2.6, 2.4 and 1.3 times their width, respectively.

Mesosoma: 1.3 times as long as high. Pronotal side rugulose dorsoposteriorly, pronotal trough crenulate, collar rugulose-punctate ventrally; rest of pronotal side smooth. Notauli deep and crenulate; mesoscutum punctulate, scutellum puncticulate. Subalar fossa foveate with carinae; precoxal sulcus crenulate-punctate; disc of mesopleuron puncticulate. Metapleuron puncticulate dorsally; rugose-reticulate ventrally. Propodeum punctulate anteriorly, rugose-reticulate posteriorly; with median longitudinal carina anteriorly and transverse carina, without distinct medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 2.2 times as long as wide; 1/R1 almost as long as stigmal length; basal posterior section of stigma 1.0 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 6.7: 2.0; m-cu: 2/Rs+M=1.6: 1; 1cu-a postfurcal, 1/Cu: 2/Cu=0.13: 1. Hindwing: r-m: 1/M=0.48: 1; 1/M: Cu&cu-a=1.9: 1.

Hind leg: Coxa rugulose dorsobasally. Lengths of femur, tibia and basitarsus 3.2, 6.7 and 4.0 times their width, respectively; tibia 1.3 times as long as femur; inner and outer spurs of tibia 0.63 and 0.50 times as long as basitarsus, respectively.

Metasoma: 1.3 times as long as wide; rugose-costate, interspace strigate; apically not incurved. T1 0.48 times as long as wide apically; basally rugose-reticulate between dorsal carina; dorsal carinae disinct anteriorly; T2+T3 0.86 times as long as wide; T3 smooth apically. Apical rim of carapace moderately emarginated. Ovipostor sheath 0.44 times as long as forewing.

Color: Black; palpi yellow, tegula dark brown. Antenna dark brown. Wings hyaline, stigma dark brown, veins yellow. Legs brownish yellow; metacoxa brownish or black dorsobasally, hind tibia (except base) and tarsus dark brown. Ovipositor sheath blackish brown.

Lengths: Body 2.2 mm, antenna 1.8 mm, forewing 2.4 mm, ovipositor sheath 1.1 mm.

Male: Unknown.

Holotype: ♀, Lienhuachih, III.1984 (KSL & KCC). Pasatype: Meifeng, 1♀, 3.V. 1983 (HT) (inAEI).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species is close to *T. tungpuensis* sp. n., but differs from it by the antenna with 20 segments, metasoma 1.3 times as long as wide, and the body black.

Etymology: *Robustus* means strong in Latin.

Triaspis (Schizoprymnus) shan sp. n.

(Figs. 16, 55, 81 107, 135, 159, 179, 202, 226, 263)

Female: Head: 1.7 times as wide as long and 1.2 times wider than mesonotum. Eye 0.90 times as long as temple. Temple and vertex puncticulate; frons punctulate laterally, strigate medioventrally, glabrate mediodorsally; without large lamellate frontal carina. POL: OD: OOL=1 : 0.75 : 2.0. Face 0.55 times as high as wide and 1.1 times as wide as eye height and 0.56 times as wide as head, densely punctate; clypeus densely punctate, distinctly concave apically, sharply pointed medially. Tentorial index 1.1. Malar space 0.69 times basal width of mandible. Antenna 24-28-segmented; F1 1.0 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.8, 3.8 and 1.3 times their width, respectively.

Mesosoma: 1.4 times as long as high. Pronotal side crenulate medially, more or less foveate posteriorly, anteroventrally rugose-punctate, rest smooth. Notauli deep and crenulate; mesoscutum punctulate, middle lobe foveate posteriorly; scutellum puncticulate. Subalar fossa foveate, with carinae; precoxal sulcus foveate; disc of mesopleuron puncticulate. Metapleuron rugose-reticulate. Propodeum rugose-reticulate; with median longitudinal carina and transverse carina, they meet to form sharp projection; without medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing: stigma 2.6 times as long as wide; 1/R1 almost as long as stigmal length; basal posterior section of stigma 1.2 times apical posterior section of stigmal; r-rs: 3+4/Rs: 2/Rs=1: 7.1: 2.7; m-cu: 2/Rs+M=1.8: 1; 1cu-a postfurcal, 1/Cu: 2/Cu=0.27: 1. Hindwing: r-m: 1/M=0.67: 1; 1/M: Cu&cu-a=1.7: 1.

Hind leg: Coxa smooth. Lengths of femur, tibia and basitarsus 3.8, 8.6 and 5.8 times their width, respectively; tibia 1.4 times as long as femur; inner and outer spurs of tibia 0.48 and 0.41 times as long as basitarsus, respectively.

Metasoma: 1.7 times as long as wide, rugose-reticulate; apicoventrally weakly incurved. T1 0.67 times as long as wide apically; dorsal carinae distinct anteriorly; T2+T3 1.1 times as long as wide. Apical rim of carapace semicircularly emarginated. Ovipositor sheath 0.34 times as long as forewing.

Color: Dark brown; palpi yellow, mesopleuron, metapleuron and propodeum lighter, metasoma brownish yellow, tegula brownish yellow. Antenna blackish brwon. Wings hyaline, stigma and veins dark brown. Legs yellow, hind tibia (except base) yellowish brown. Ovipositor sheath dark brown.

Lengths: Body 3.4 mm, antenna 2.9 mm, forewing 2.9 mm, ovipositor sheath 1.0 mm.

Male: Unknown.

Holotype: ♀, Lienhuachih, IX.1984 (KSL & KCC). Paratypes: Lienhuachih, 1♀, VIII, & 6♀, IX.1984 (KSL & KCC). Meifeng, 1♀, 15.VII. 1982 (SCL & CNL). Tungpu, 1♀, 20-24.

1983 (KCC & CYW); 1♀, 23-27.VII.1984 (KCC & CHY). Wufeng, 1♀, 7-11.VII.1979 (KCC). Wuling, 2♀, 27-29.VI.1979 (KSL & LYC).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species differs from the other Taiwanese *Triaspis* species by the following combination of characters: vein 1/R1 of forewing almost as long as stigmal length, clypeus concave apically and sharply pointed medially, metasoma 1.7 times as long as wide, and carapace apicoventrally weakly incurved.

Etymology: The specific name is the Chinese noun "shan" (mountain). It refers to the shape of apical clypeus.

Triaspis (Schizoprymnus) tungpuensis sp. n.

(Figs. 22, 56, 82 108, 136, 160, 175, 201, 229, 264)

Female: Head: 1.8 times as wide as long and 1.2 times wider than mesonotum. Eye 1.1 times as long as temple. Temple puncticulate; frons punctulate laterally, glabrous medially, rugose-punctate submedially; without large lamellate frontal carina. POL: OD: OOL=1 : 0.83 : 2.3. Vertex puncticulate, densely punctate around ocelli. Face 0.47 times as high as wide and 1.2 times as wide as eye height and 0.60 times as wide as head; densely punctate, with rugae near toruli; clypeus densely punctate, almost straight apically, not sharply pointed medially. Tentorial index 0.57. Malar space 0.73 times basal width of mandible. Antenna 23-segmented; F1 1.0 times as long as F2; lengths of F1, F2 and penultimate flagellomers 3.3, 3.3 and 1.3 times their width, respectively.

Mesosoma: 1.4 times as long as high. Pronotal side largely smooth, medioanterioly crenulate, posteriorly foveate. Notauli deep and crenulate; mesoscutum punctulate, scutellum puncticulate. Subalar fossa foveate, with carinae posteriorly, precoxal sulcus foveate-rugose; disc of mesopleuron puncticulate. Metapleuron rugose-reticulate, sculptures weaker dorsally. Propodeum rugose-reticulate anteriorly, posteromedially weakly rugose-reticulate, rather smoot posterolaterally; with median longitudinal carina anteriorly and transverse carina, with ill defined medioposterior area; lateral propodeal tubercles distinct.

Wings: Forewing stigma 2.2 times as long as wide, 1/R1 almost as long as stigmal length; basal posterior section of stigma 1.2 times apical posterior section of stigmal; r-rs: 3+4/Rs: 2/Rs=1: 11.0: 4.0; m-cu: 2/Rs+M=2.1: 1; 1cu-a postfurcal, 1/Cu: 2/Cu=0.26: 1. Hindwing: r-m: 1/M=0.70: 1; 1/M: Cu&cu-a=1.7: 1.

Hind leg: Coxa smooth. Lengths of femur, tibia and basitarsus 3.5, 6.8 and 4.3 times their width, respectively; tibia 1.3 times as long as femur; inner and outer spurs of tibia 0.59 and 0.53 times as long as basitarsus, respectively.

Metasoma: 1.5 times as long as wide; rugose-costate, interspace strigate; apically not incurved. T1 0.63 times as long as wide apically; basally rugose-reticulate between dorsal carinae; dorsal carinae distinct basally; T2+T3 almost as long as wide. Apical rim of carapace strongly emarginated. Ovipostior sheath 0.48 times as long as forewing.

Color: Dark brown; palpi and tegula brownish yellow. Antenna dark brown. Wings

hyaline, stigma and veins dark brown. Legs brownish yellow; hind tibia (except base) and tarsus dark brown. Ovipositor sheath blackish brown.

Lengths: Body 2.4 mm, antenna 2.2 mm, forewing 2.5 mm, ovipositor sheath 1.2 mm.

Male: Unknown.

Holotype: ♀, Tungpu, 28.IV.-2.V.1981 (TL & CJL). Paratype:Wushe, 1♀, 26.1V.1983 (HT) (in AEI).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species is close to *T. robustus* sp. n., but differs from it by the antenna with 23 segments, metasoma 1.5 times as long as wide, and the body dark brown.

Etymology: The specific name is derived from the name of the type locality, Tungpu.

Subgenus *TRIASPIS* Haliday

Triaspis Haliday, 1835. Ent. Mag. 3: 124, as subgenus of *Helcon.* Type species: *Sigalphus caudatus* Nees; designated by Viereck, 1912. - Viereck, 1912. Proc. U.S. natn. Mus. 42: 628.

Ichneutipterus Vachal, 1907. Revue Ent. 26: 122. Type species: *Sigalphus ? ichneutipterus* Vachal, by monotype.

Triaspis (*Triaspis*): Martin, 1956. Publ. Dep. Agric. Can. 965: 64.

The subgenus *Triaspis* is characterized by the following combination of characters: propodeum without distinct spines; carapace with 2 distinct sutures; rim of carapace behind not denticulate. It contains about 110 species in the world. In this paper 2 new species are described from Taiwan.

Key to species of the subgenus *Triaspis* from Taiwan

1. Clypeus sharply pointed medially; carapace apically not incurved·········*shangchia* sp. n.

-. Clypeus not sharply pointed medially; carapace apicoventrally somewhat incurved ······ ··· *concavus* sp. n.

Triaspis (Triaspis) concavus sp. n.

(Figs. 33, 57, 83, 109, 111, 161, 187, 213, 239, 266)

Female: Head: 1.7 times as wide as long and 1.3 times wider than mesonotum, punctulate. Eye 1.5 times as long as temple. Frons rugose medioventrally, frontal carina distinct ventrally. POL: OD: OOL=1 : 0.73: 1.6. Face 0.56 times as high as wide and 1.2 times as wide as eye height and 0.58 times as wide as head; clypeus concave medially, not sharply pointed medially. Tentorial index 0.82. Malar space 1.0 times basal width of mandible. Antenna 23-segmented; F1 0.93 times as long as F2; lengths of F1, F2 and penultimate flagellomere 3.5, 3.8 and 1.0 times their width, respectively.

Mesosoma: 1.4 times as long as high. Pronotal side reticulate anteroventrally, medially and posteriorly, rest of pronotal side smooth. Notauli deep and crenulate; mesoscutum

punctulate; scutellum puncticulate. Subalar fossa and precoxal sulcus foveate; pleural groove crenulate, disc of mesopleuron largely puncticulate. Metapleuron reticulate-rugose. Propodeum largely rugose-reticulate, rather smooth anteriorly; with median longitudinal carina anteriorly and shortly developed transverse carina, without medioposterior area; lateral propodeal tubercles rather distinct.

Wings: Forewing: stigma 2.7 times as long as wide; 1/R1 slighly longer than stigmal length; basal posterior section of stigma 1.2 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 9.2: 3.2; m-cu: 2/Rs+M=1.9: 1; 1cu-a postfurcal, 1/Cu: 2/Cu=0.15 : 1. Hindwing: r-m: 1/M=0.50: 1 ; 1/M: Cu&cu-a=2.2: 1.

Hind leg: Coxal largely smooth. Lengths of femur, tibia and basitarsus 4.2, 8.3 and 6.0 times their width, respectively; tibia 1.4 times as long as femur; inner and outer spurs of tibia 0.29 and 0.25 times as long as basitarsus, respectively.

Metasoma: 1.7 times as long as wide, costate-rugulose, interspace strigate, apicoventrally somewhat incruved. T1 0.65 times as long as wide apically; dorsal carinae rather distinct in basa half; T2+T3 1.2 times as long as wide. Apical rim of carapace moderately emarginated. Ovipositor sheath 0.44 times as long as forewing.

Color: Blackish brown; palpi yellow, tegula yellowish brown. Antenna yellowish brown basally, dark brown apically. Wings hyaline, stigma and veins dark brown. Legs yellowish brown, hind tibia dark brown. Ovipositor sheath dark brown.

Lengths: Body 2.4 mm, antenna 1.9 mm, forewing 2.2 mm, ovipositor sheath 0.98 mm.

Male: Unknown.

Holotype: ♀, Lienhuachih, V.1984 (KSL & KCC). Paratypes: Lienhuachih, 1♀, same data as holotype. Wangfeng, IV.1984 (KSL & KCC). Wushe, 1♀, 22.V.1983 (HT) (in AEI).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species differs from *T. shangchia* sp. n, by the clypeus not sharply pointed medially; basal flagellomeres distinctly lighter than apical segments, F1 3.5 times as long as wide; carapace apicoventrally somewhat incurved.

Etymology: *Concavus* means concave in Latin, refers to its clypeus concave medially.

Triaspis (Triaspis) shangchia sp. n.

(Figs. 34, 58, 84 110, 112, 162, 188, 214, 240, 265)

Female: Head: 1.4 times as wide as long and 1.2 times wider than mesonotum. Eye 0.70 times as long as temple. Temple, frons and vertex puncticulate; frons glabrous medioventrally; without distinct frontal carina. POL: OD: OOL=1 : 0.45 : 1.5. Face 0.60 times as high as wide and 1.1 times as wide as eye height and 0.56 times as wide as head, punctulate; clypeus sparsely punctate dorsally, rugulose ventrally, sharply pointed medially. Tentorial index 1.0. Malar space 0.82 times basal width of mandible. Antenna 29-segmented; F1 0.90 times as long as F2; lengths of F1, F2 and penultimate flagellomere 4.8, 4.2 and 1.3 times their width, respectivly.

Mesosoma: 1.5 times as long as high. Pronotal side largely smooth; pronotal trough

crenulate, collar anterially with some punctures and rugosity. Notauli deep and crenulate; mesoscutum punctulate, middle lobe with some rugulose posteriorly; scutellum puncticulate. Subalar fossa with some punctures and rugosity, precoxal sulcus crenulate; pleural groove crenulate, disc of mesopleuron puncticulate. Metapleuron rugose-reticulate. Propodeum punctulate anteriorly, rugose-reticulate posteriorly; with median longitudinal carina anteriorly and ill defined transverse carina, without distinct medioposterior area; without distinct lateral propodeal tubercles.

Wings: Forewing: stigma 2.8 times as long as wide; 1/R1 almost as long as stigmal length; basal posterior section of stigma 1.2 times apical posterior section of stigma; r-rs: 3+4/Rs: 2/Rs=1: 7.6: 2.4; m-cu: 2/Rs+M=1.6: 1; 1cu-a postfurcal, 1/Cu: 2/Cu=0.19 : 1. Hindwing: r-m: 1/M=0.48: 1; 1/M: Cu&cu-a=1.6: 1.

Hind leg: Coxa with carinae dorsally. Lengths of femur, tibia and basitarsus 5.1, 9.0 and 8.0 times their width, respectively; tibia 1.4 times as long as femur; inner and outer spurs of tibia subequal, 0.38 times as long as basitarsus.

Metasoma: 1.7 times as long as wide; costate-rugulose, interspace strigulate or rugulose; apically not incurved. T1 0.63 times as long as wide apically; dorsal carinae rather distinct in basal half; T2+T3 1.1 times as long as wide. Apical rim of carapace weakly emarginated. Ovipositor sheath 0.67 times as long as forewing.

Color: Black; palpi and tegula blackish brown. Antenna blackish brown. Wings hyaline, stigma and veins dark brown. Legs dark brown; fore coxa, hind tibia and tarsus blackish brown, middle and metacoxae blackish brown. Ovipositor sheath blackish brown.

Lengths: Body 3.2 mm, antenna 3.1 mm, forewing 3.3 mm, ovipositor sheath 2.2 mm.

Male: Unknown.

Holotype: ♀, Tayulilng, 10-16.VI.1980 (KSL & BHC).

Distribution: Taiwan.

Host: Unknown.

Remarks: This species differs from *T. concavus* sp. n, by the clypeus sharply pointed medially; basal flagellomeres concolor with apical segments, F1 4.8 times as long as wide; carapace apically not incurved.

Etymology: The specific name is the Chinese noun "shangchia" (temple). It refers to the temple distinctly longer than eye length.

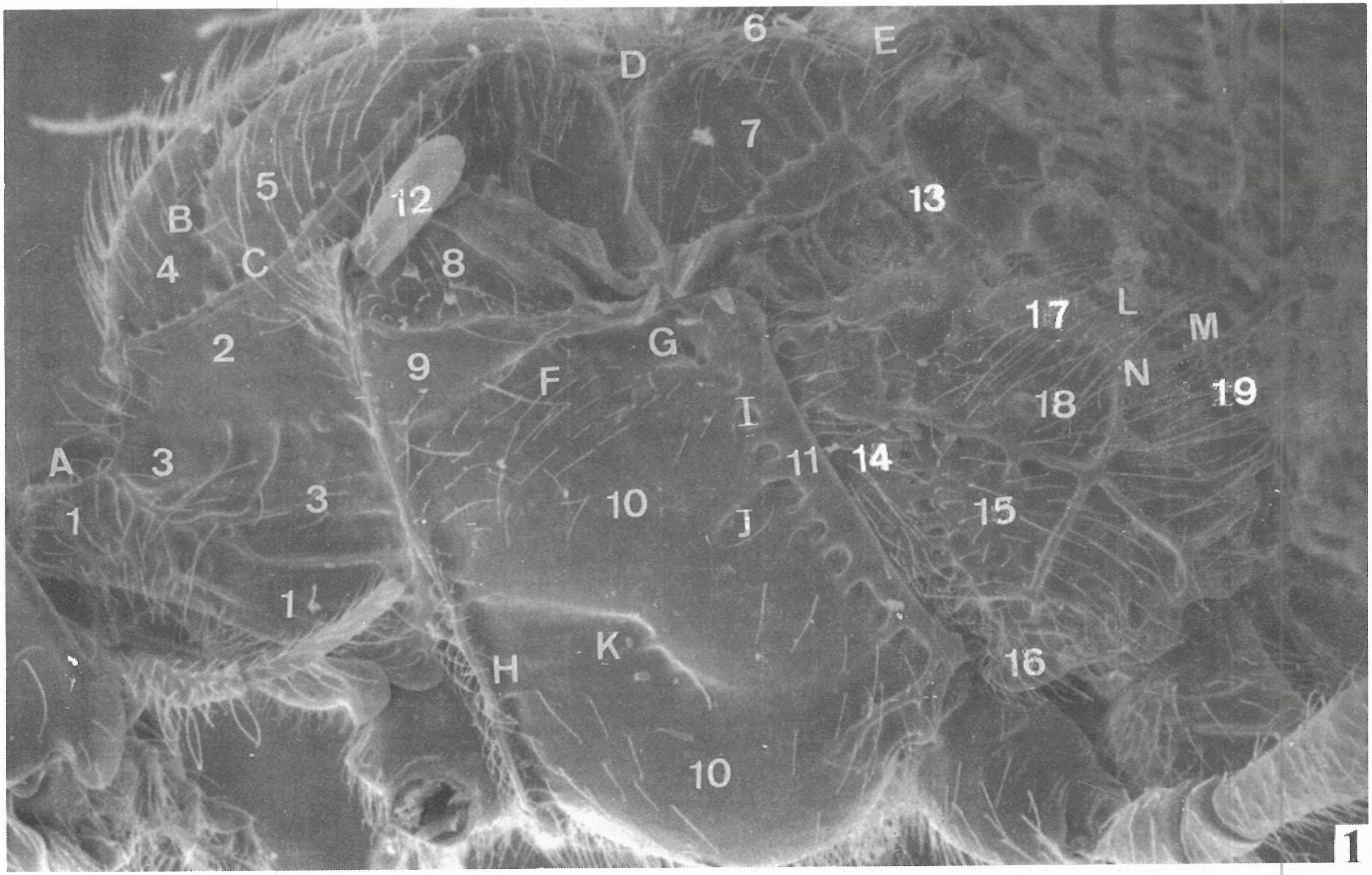


Fig. 1. Mesosoma in lateral view of *Blacus comatus* Van Achterberg.: 1, Collar; 2, Dorsal part of pronotal side; 3, Pronotal trough; 4, Midle lobe of mesoscutum; 5, Lateral lobe of mesoscutum; 6, Scutellum; 7, Axillary trough of mesonotum; 8, Anterior subalar depresson; 9, Subalar prominence; 10, Mesepistermum; 11, Mesepimeron; 12, Tegula; 13, Dorsellum; 14, Metepisternum; 15, Metepimeron; 16, Metapleural flange; 17, Propodeum; 18, Propodeal spiracle; 19, Areola; A, Pronope; B, Notauli; C, Lateral carina of mesoscutum; D, Scuto-scutellar sulcus; E, Lateral carina of scutellum; F, Subalar fossa; G, Subalar pit; H, Epicnemial carina; I, Pleural groove; J, Epistenal scrobe; K, Precoxal sulcus; L, Mediolongitudinal carina; M+N, Basal transverse carina; N, Costula.

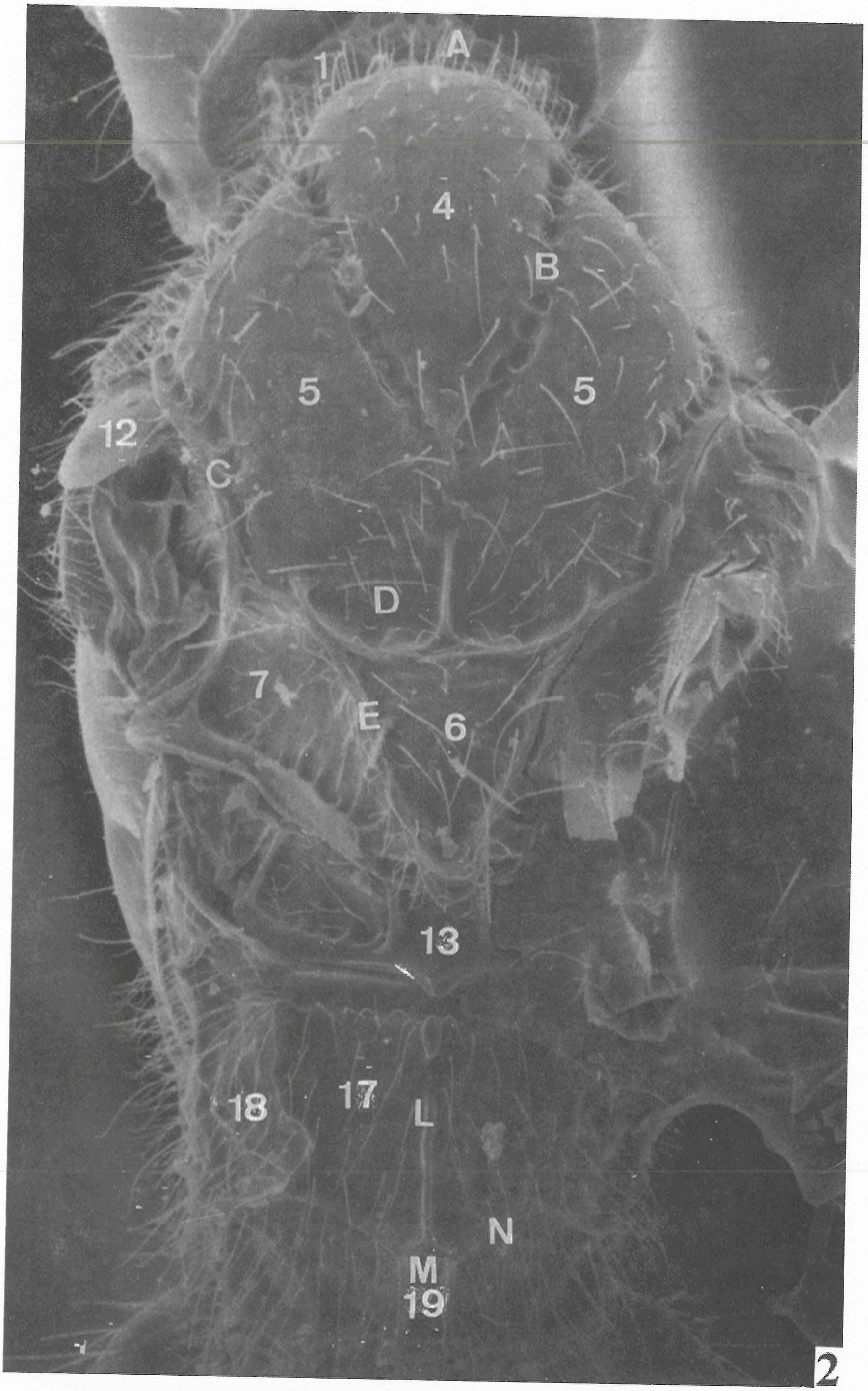
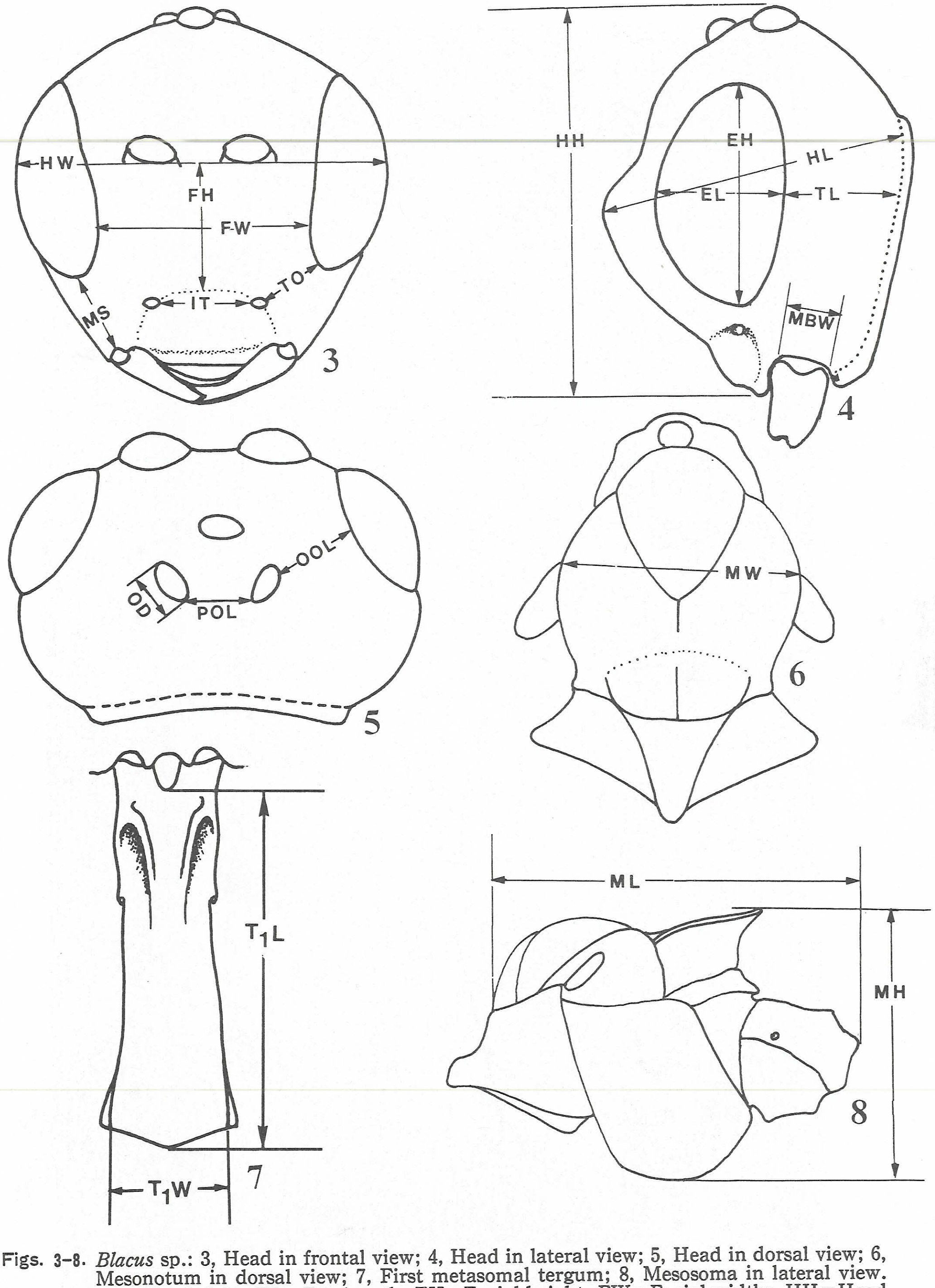
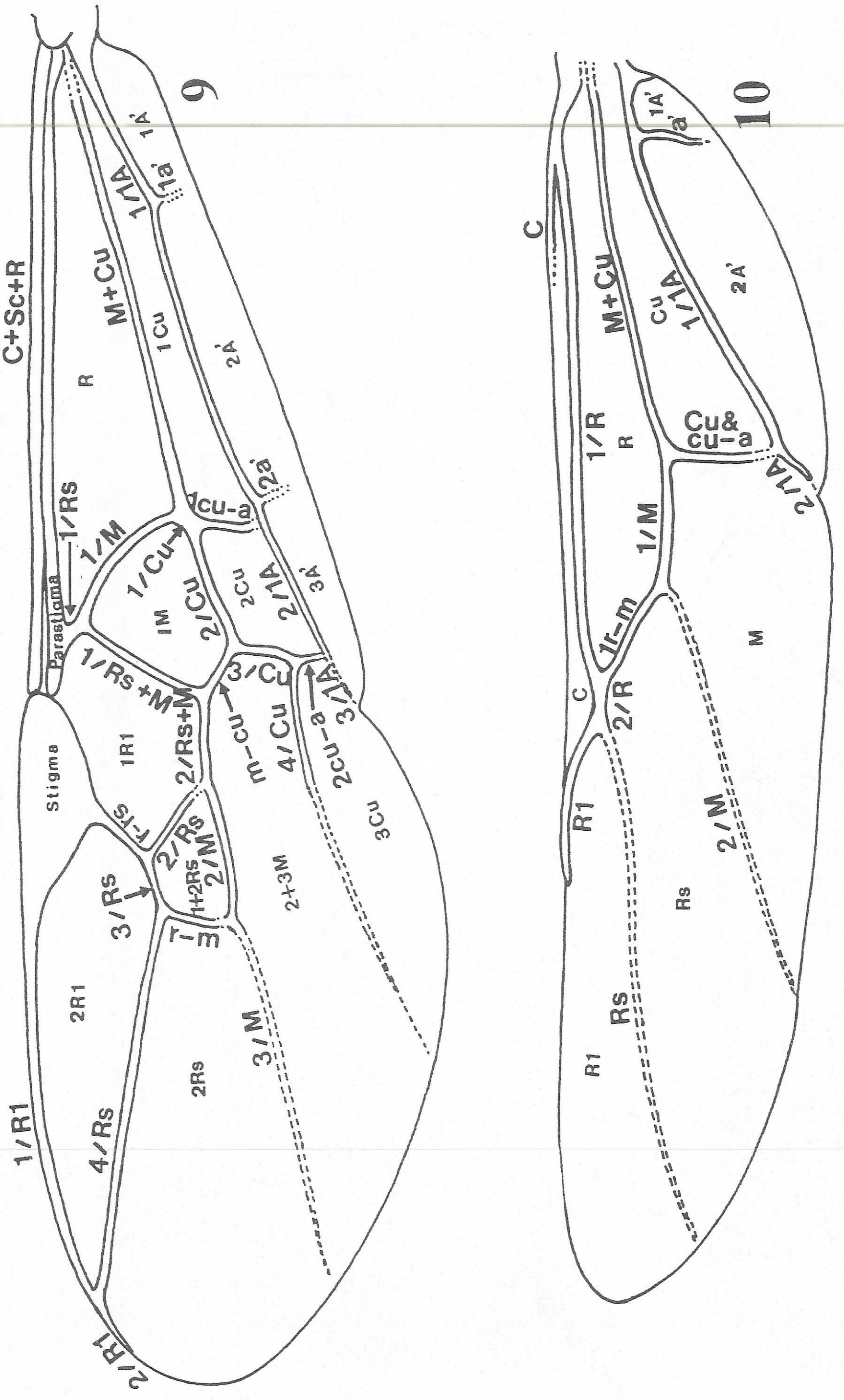


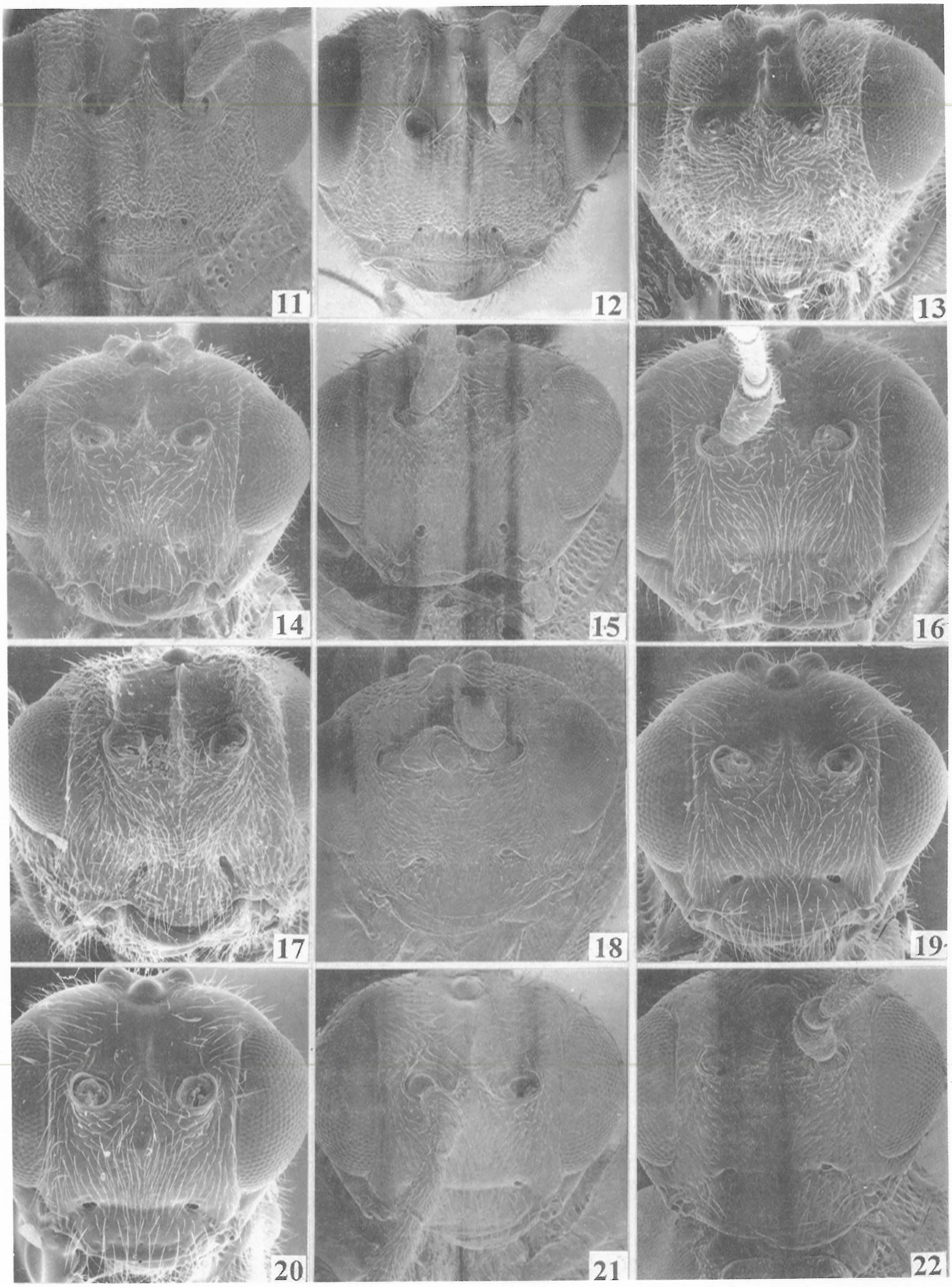
Fig. 2. Mesosoma in dorsal view of *Blacus comatus* Van Achterberg. 4, Middle lobe of mesoscutum; 5, Lateral lobe of mesoscutum; 6, Scutellum; 7, Axillary trough of mesonotum; 12, Tegula; 13, Dorsellum; 17, Propodeum; 18, Propodeal spiracle; 19, Areola; B, Notauli; C, Lateral carina of mesoscutum; D, Scuto-scutellar sulcus; E, Lateral carina of scutellum; L, Mediolongitudinal carina; M+N, Basal transverse carina; N, Costula.



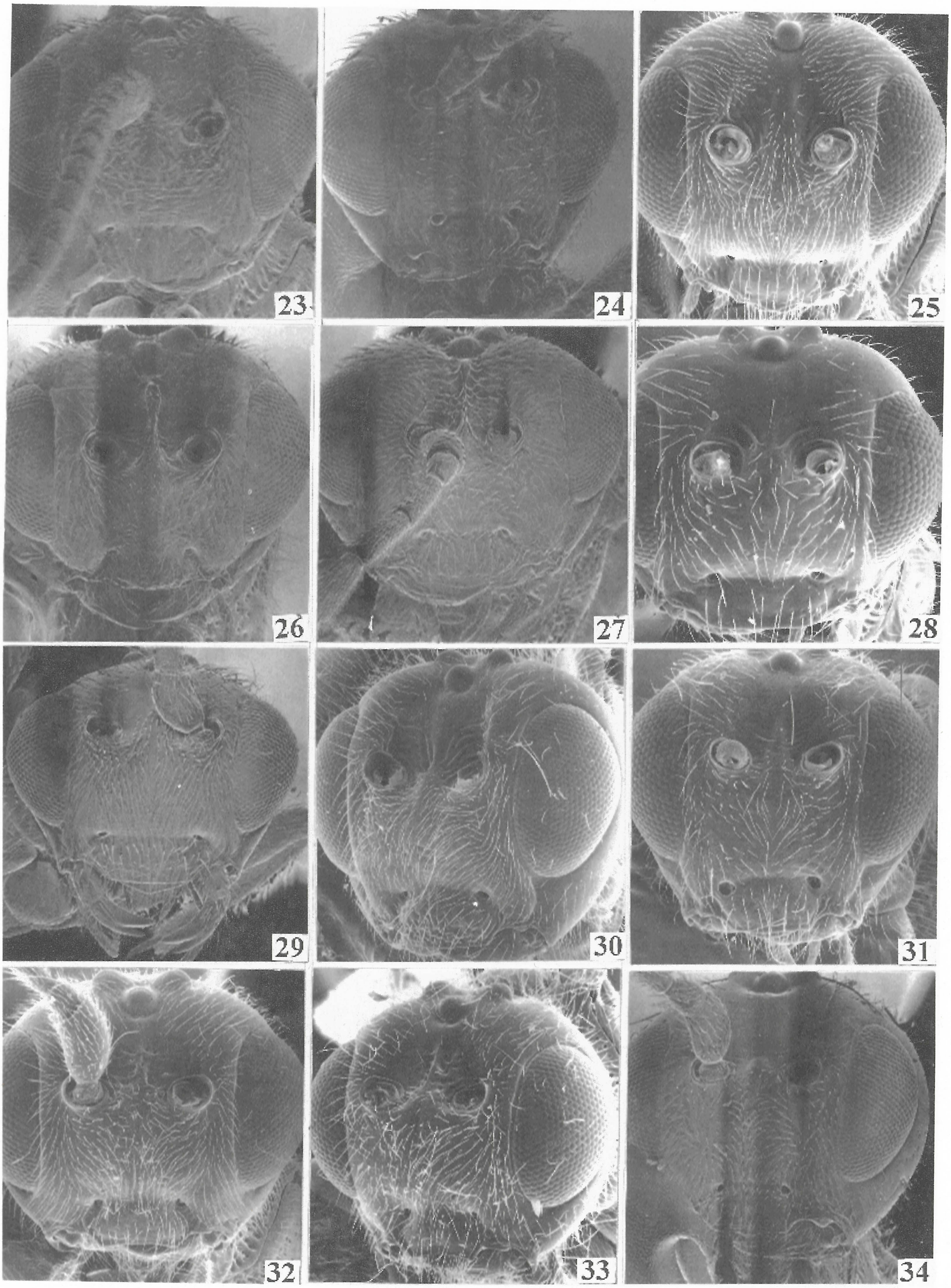
Figs. 3–8. *Blacus* sp.: 3, Head in frontal view; 4, Head in lateral view; 5, Head in dorsal view; 6, Mesonotum in dorsal view; 7, First metasomal tergum; 8, Mesosoma in lateral view. EH=Eye height; EL=Eye length; FH=Facial height; FW=Facial width; HH=Head height; HL=Head length; HW=Head width; IT =Intertentorial line; MBW=Mandible width; MH = Mesosomal height; ML = Mesosomal length; MS = Malar space; MW=Mesosomal width; OD=Ocellar diameter; OOL=ocular ocellar line; POL=posterior ocellar line; TL=Temple length; TO=Tentorio-ocular line; T1L=First metasomal tergite length; T1W=First metasomal tergite width.



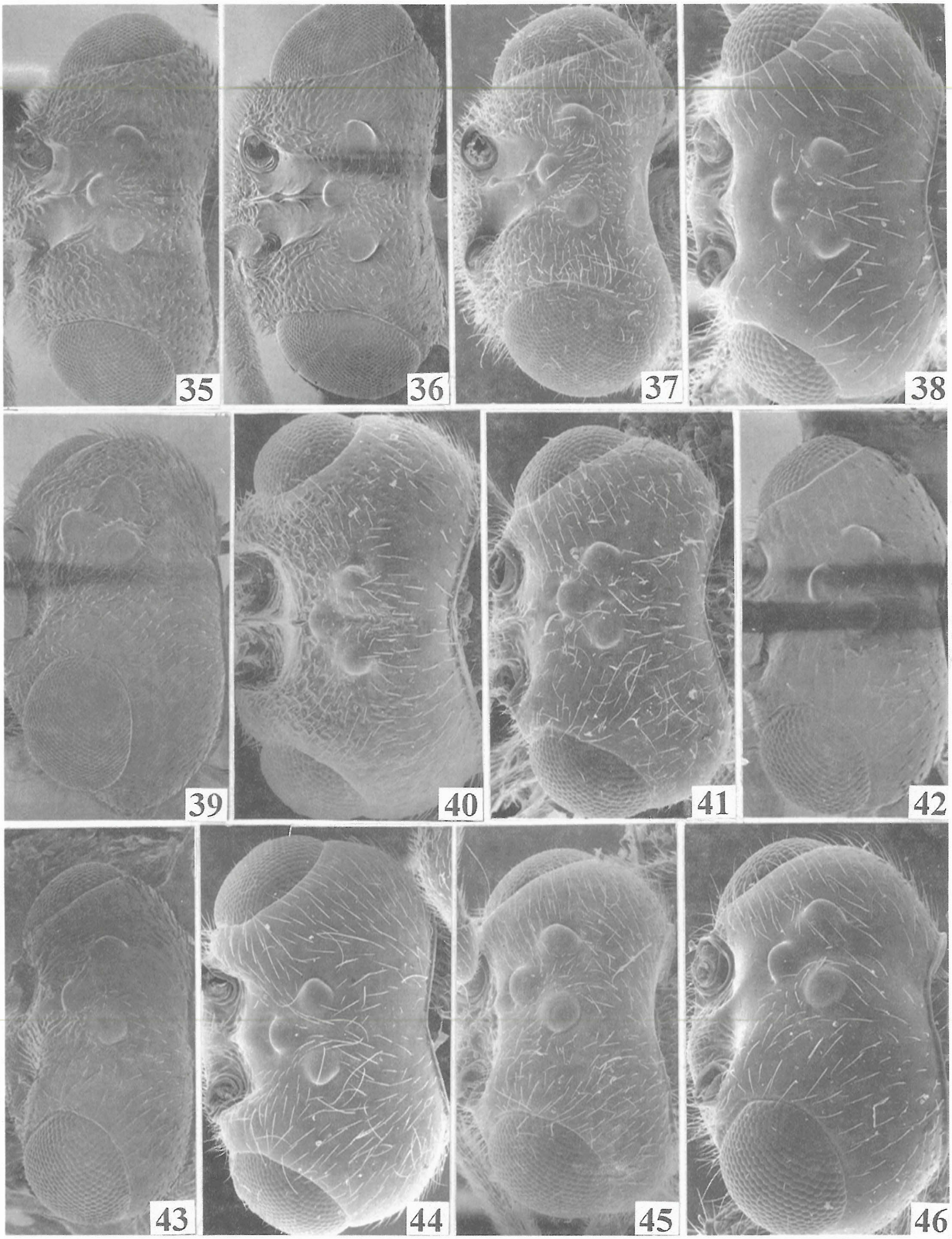
Figs. 9–10. Nomenclature of the wing venation (After Huber and Sharkey, 1993): 9, Forewing; 10, Hindwing.



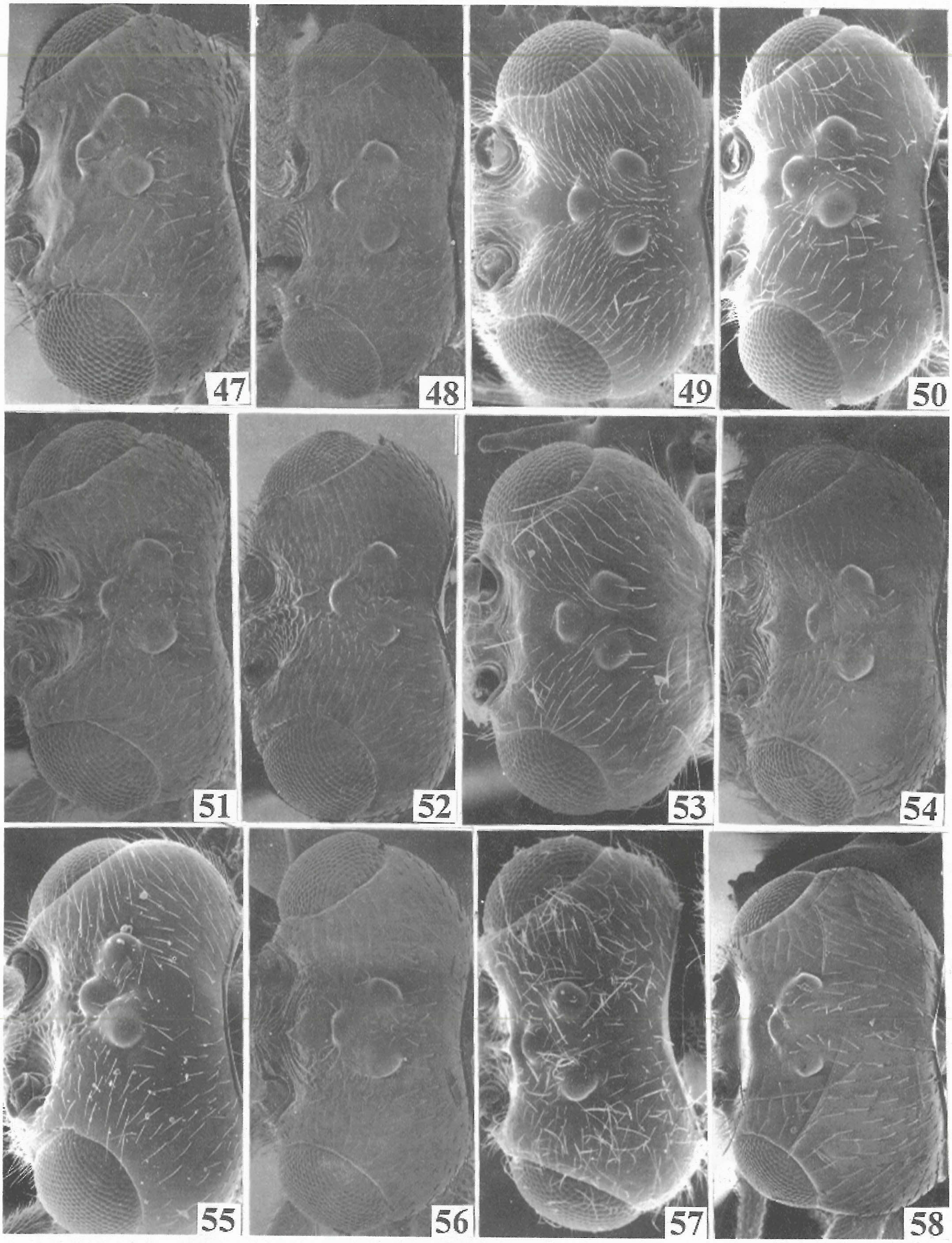
Figs. 11–22. Frontal view of heads of Triaspina ♀: 11, *Canalicephalus fugou* sp. n.; 12, *C. longus* sp. n.; 13, *C. taiwanensis* sp.n.; 14, *Triaspis imitatus* Papp; 15, *T. hui* sp. n.; 16, *T. shan* sp. n.; 17, *T. borpian* sp.n.; 18, *T. bicolor* sp.n.; 19, *T. distinctus* sp.n.; 20, *T. kueichia* sp.n.; 21, *T. robustus* sp.n.; 22, *T. tungpuensis* sp.n.



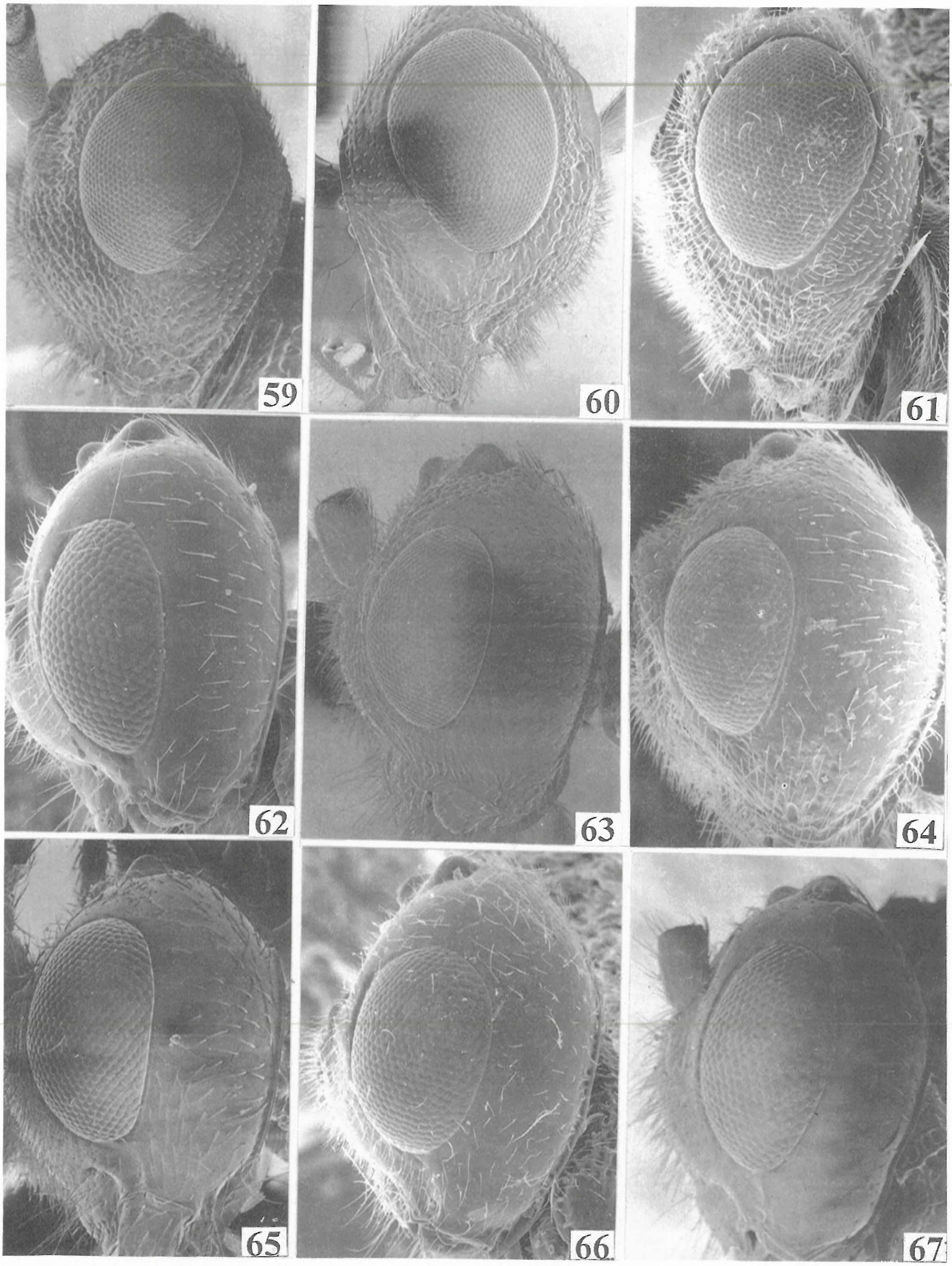
Figs. 23–34. Frontal view of heads of Triaspina ♀: 23, *Triaspis chouwen* sp. n.; 24, *T. fessus* sp. n.; 25, *T. ketiao* sp. n.; 26, *T. lienhuachihensis* sp. n.; 27, *T. loi* sp. n.; 28, *T. beitun* sp. n.; 29, *T. calvus* sp. n.; 30, *T. chunji* sp. n.; 31, *T. ovatus* sp. n.; 32, *T. curvatus* sp. n.; 33, *T. concavus* sp. n.; 34, *T. shangchia* sp. n.



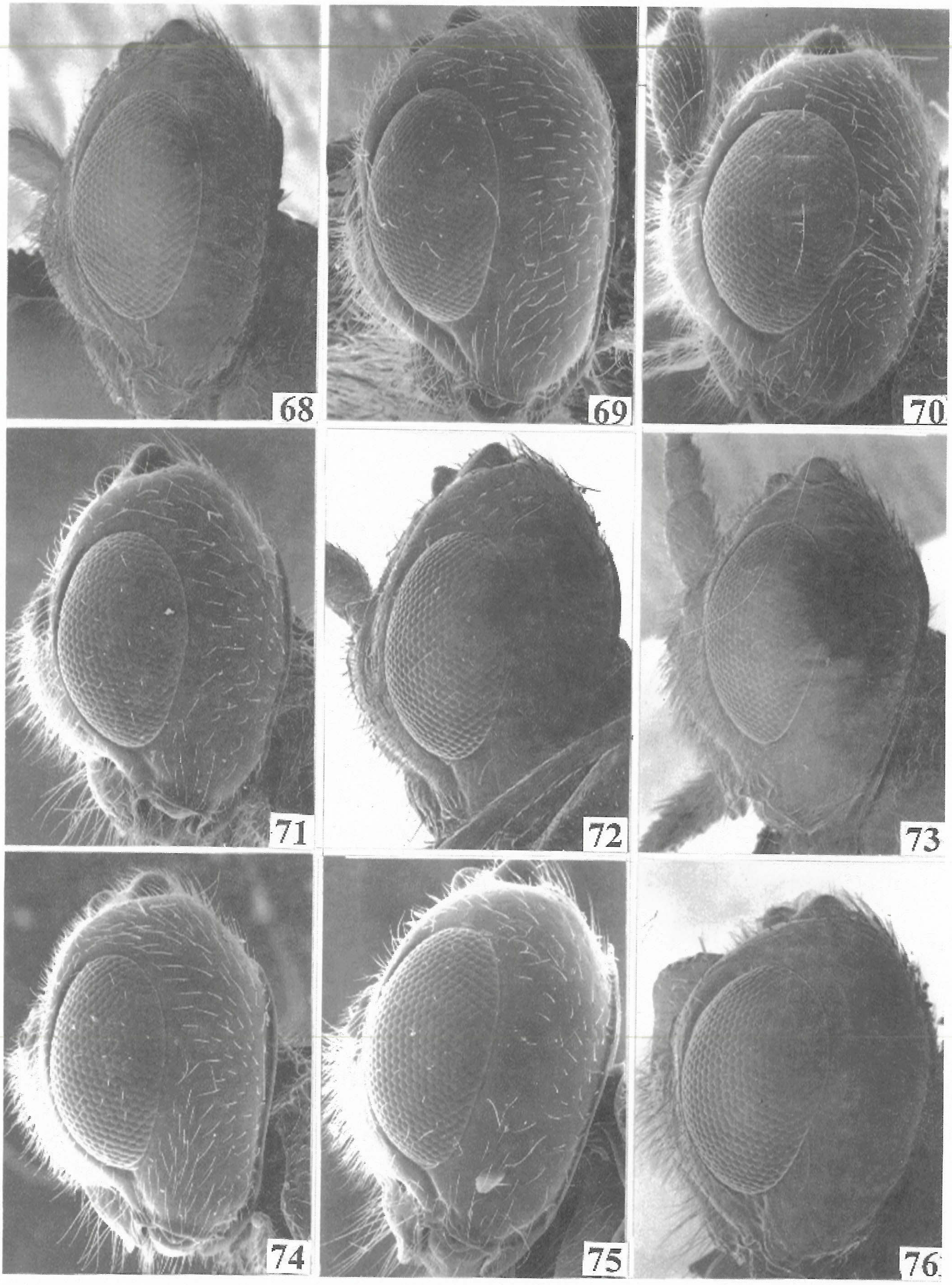
Figs. 35–46. Dorsal view of heads of Triaspina ♀: 35, *Canalicephalus fugou* sp. n.; 36, *C. longus* sp. n.; 37, *C. taiwanensis* sp. n.; 38, *Triaspis beitun* sp. n.; 39, *T. bicolor* sp. n.; 40, *T. borpian* sp. n.; 41, *T. imitatus* Papp; 42, *T. chiu* sp. n.; 43, *T. chouwen* sp. n.; 44, *T. chunji* sp. n.; 45, *T. curvatus* sp. n.; 46, *T. distinctus* sp. n.



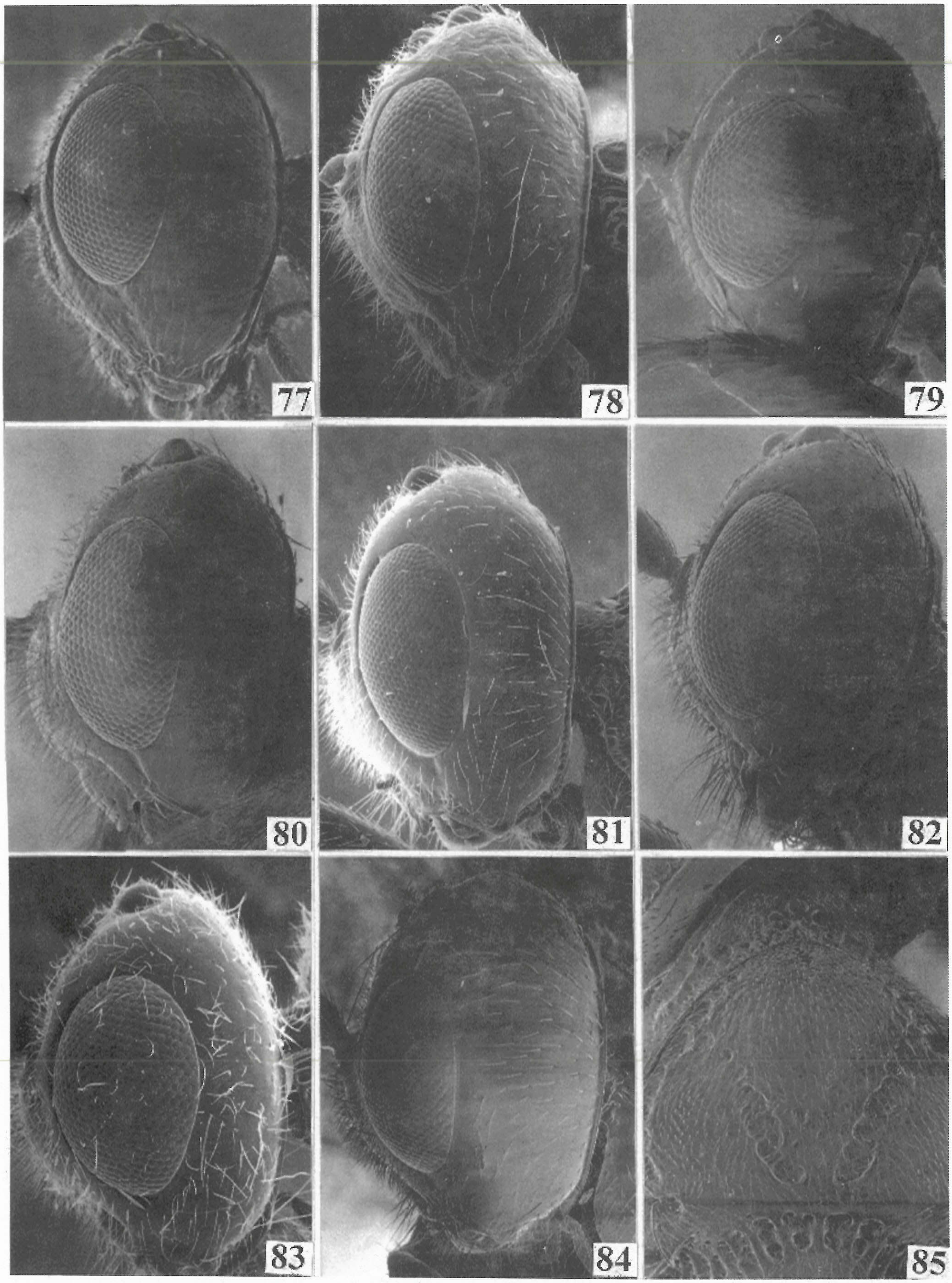
Figs. 47–58. Dorsal view of heads of Triaspina ♀: 47, *Triaspis fessus* sp. n.; 48, *T. hui* sp. n.; 49, *T. ketiao* sp. n.; 50, *T. kueichia* sp. n.; 51, *T. lienhuachihensis* sp. n.; 52, *T. loi* sp. n.; 53, *T. ovatus* sp. n.; 54, *T. robustus* sp. n.; 55, *T. shan* sp. n.; 56, *T. tungpuensis* sp. n.; 57, *T. concavus* sp. n.; 58, *T. shangchia* sp. n.



Figs. 59–67. Lateral view of heads of Triaspina ♀: 59, *Canalicephalus fugou* sp. n.; 60, *C. longus* sp. n.; 61, *C. taiwanensis* sp. n.; 62, *Triaspis beitun* sp. n.; 63, *T. bicolor* sp. n.; 64, *T. borpian* sp. n.; 65, *T. calvus* sp. n.; 66, *T. imitatus* Papp; 67, *T. chiu* sp.n.

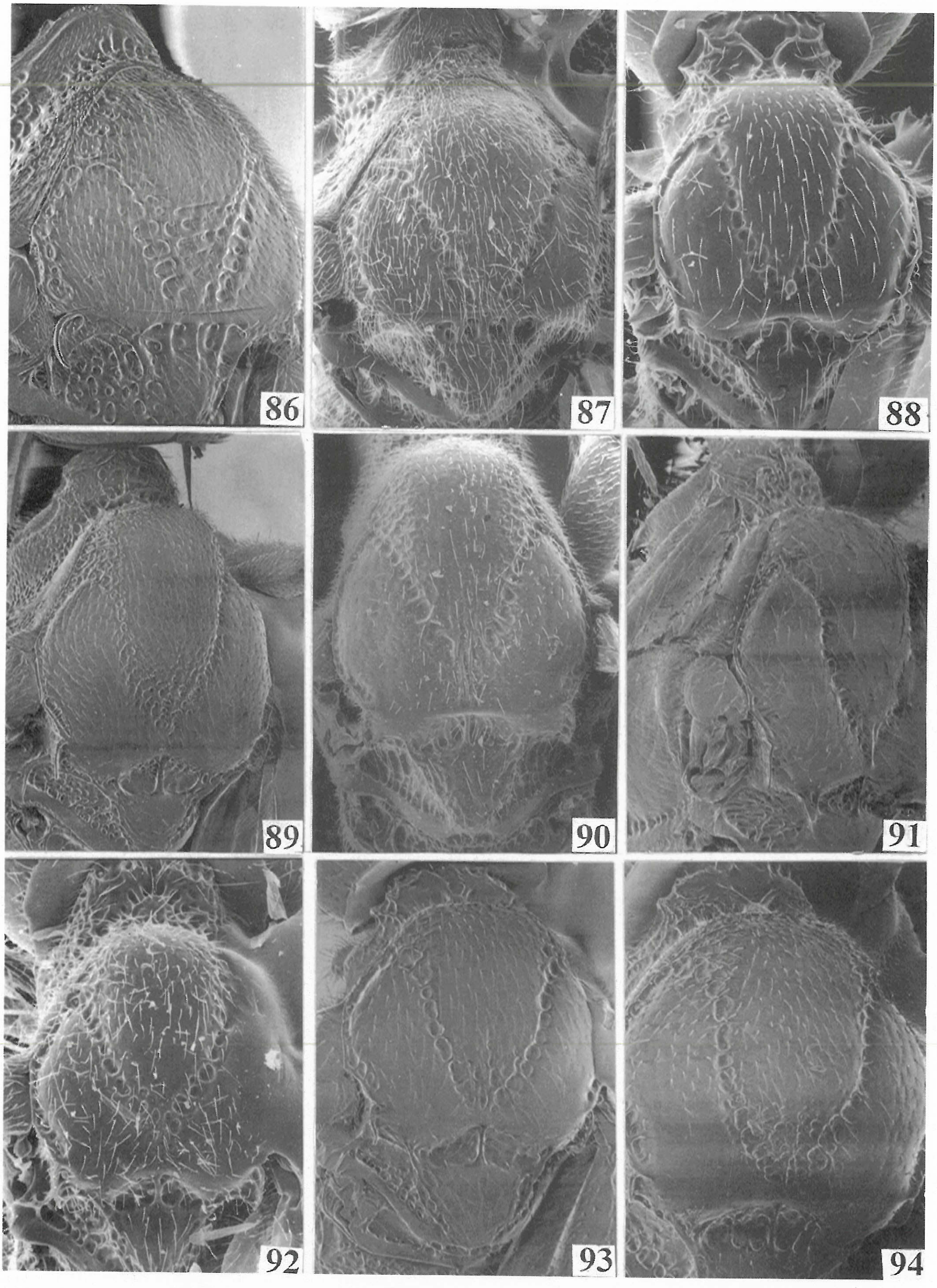


Figs. 68–76. Lateral view of heads of Triaspina ♀: 68, *Triaspis chouwen* sp. n.; 69, *T. chunji* sp. n.; 70, *T. curvatus* sp. n.; 71, *T. distinctus* sp. n.; 72, *T. fessus* sp. n.; 73, *T. hui* sp. n.; 74, *T. ketiao* sp. n.; 75, *T. kueichia* sp. n.; 76, *T. lienhuachihensis* sp. n.

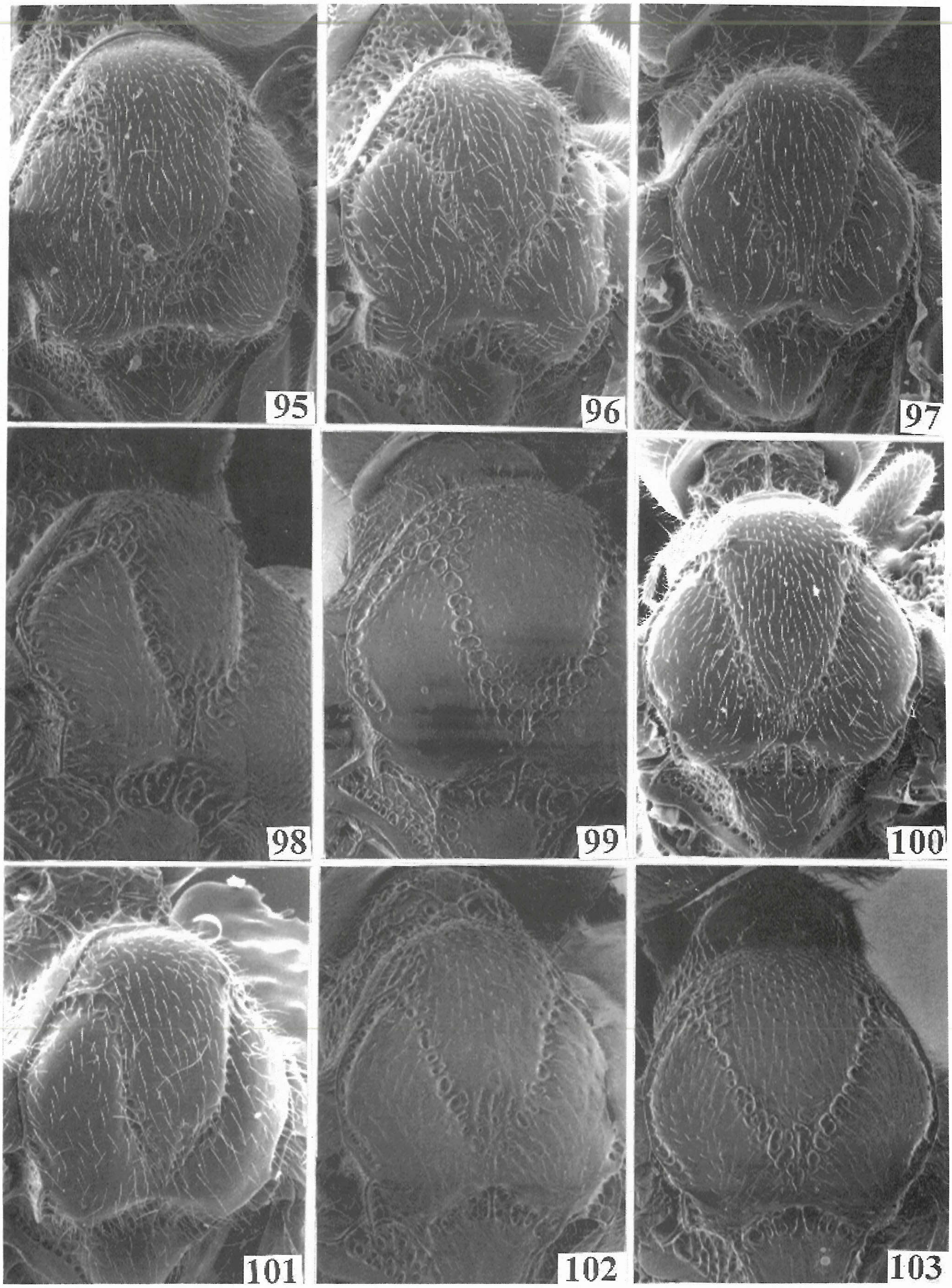


Figs. 77–84. Lateral view of heads of Triaspina ♀: 77, *Triaspis loi* sp. n.; 78, *T. ovatus* sp. n.; 79, *T. plenus* sp. n.; 80, *T. robustus* sp. n.; 81, *T. shan* sp. n.; 82, *T. tungpuensis* sp. n.; 83, *T. concavus* sp. n.; 84, *T. shangchia* sp. n.

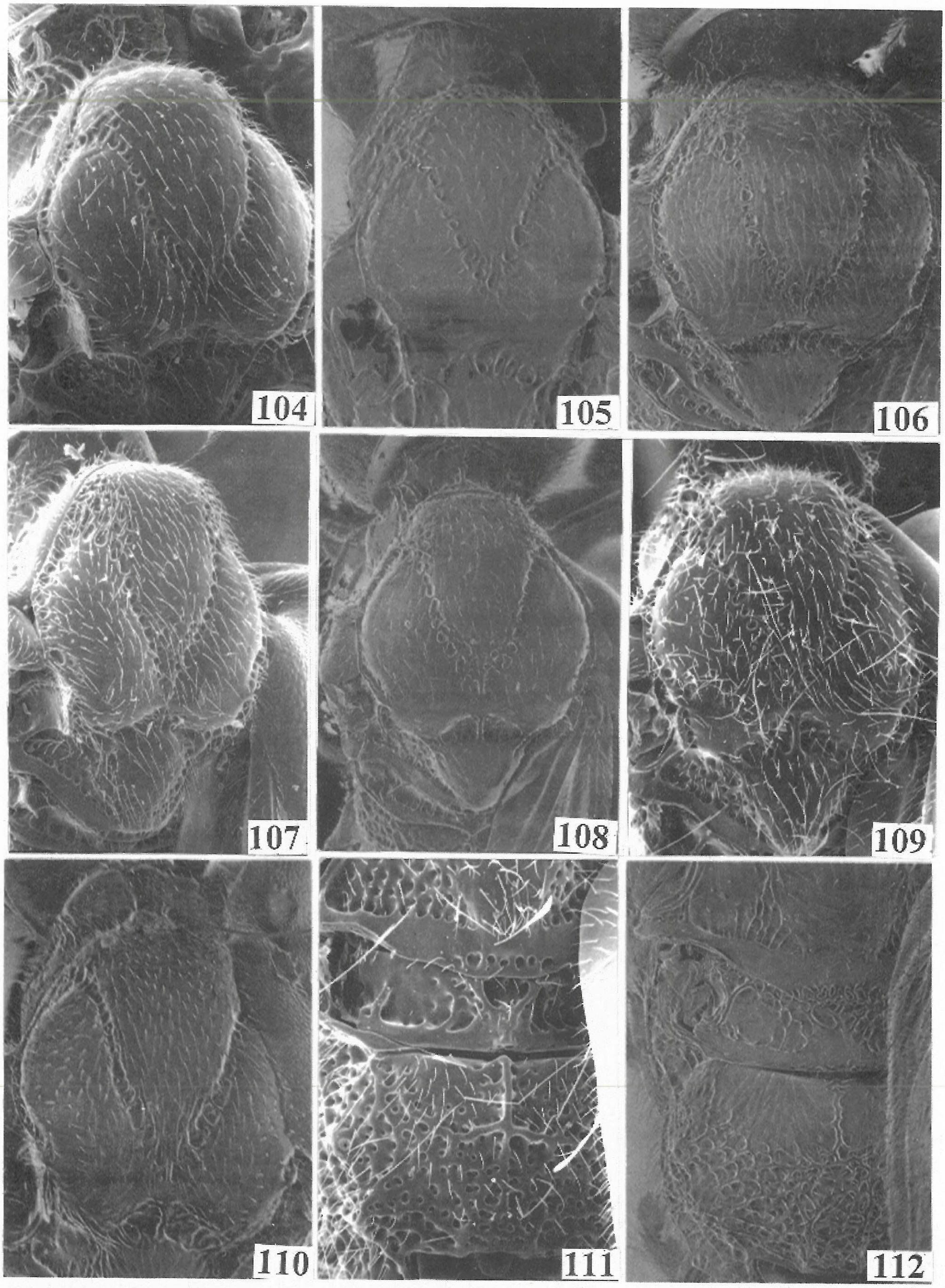
Fig. 85. Dorsal view of mesoscutum of *Canalicephalus fugou* sp. n.♀.



Figs. 86–94. Dorsal view of mesonota of Triaspina ♀: 86, *Canalicephalus longus* sp. n.; 87, *C. taiwanensis* sp. n.; 88, *Triaspis beitun* sp. n.; 89, *T. bicolor* sp. n.; 90, *T. borpian* sp. n.; 91, *T. calvus* sp. n.; 92, *T. imitatus* Papp; 93, *T. chiu* sp. n.; 94, *T. chouwen* sp. n.

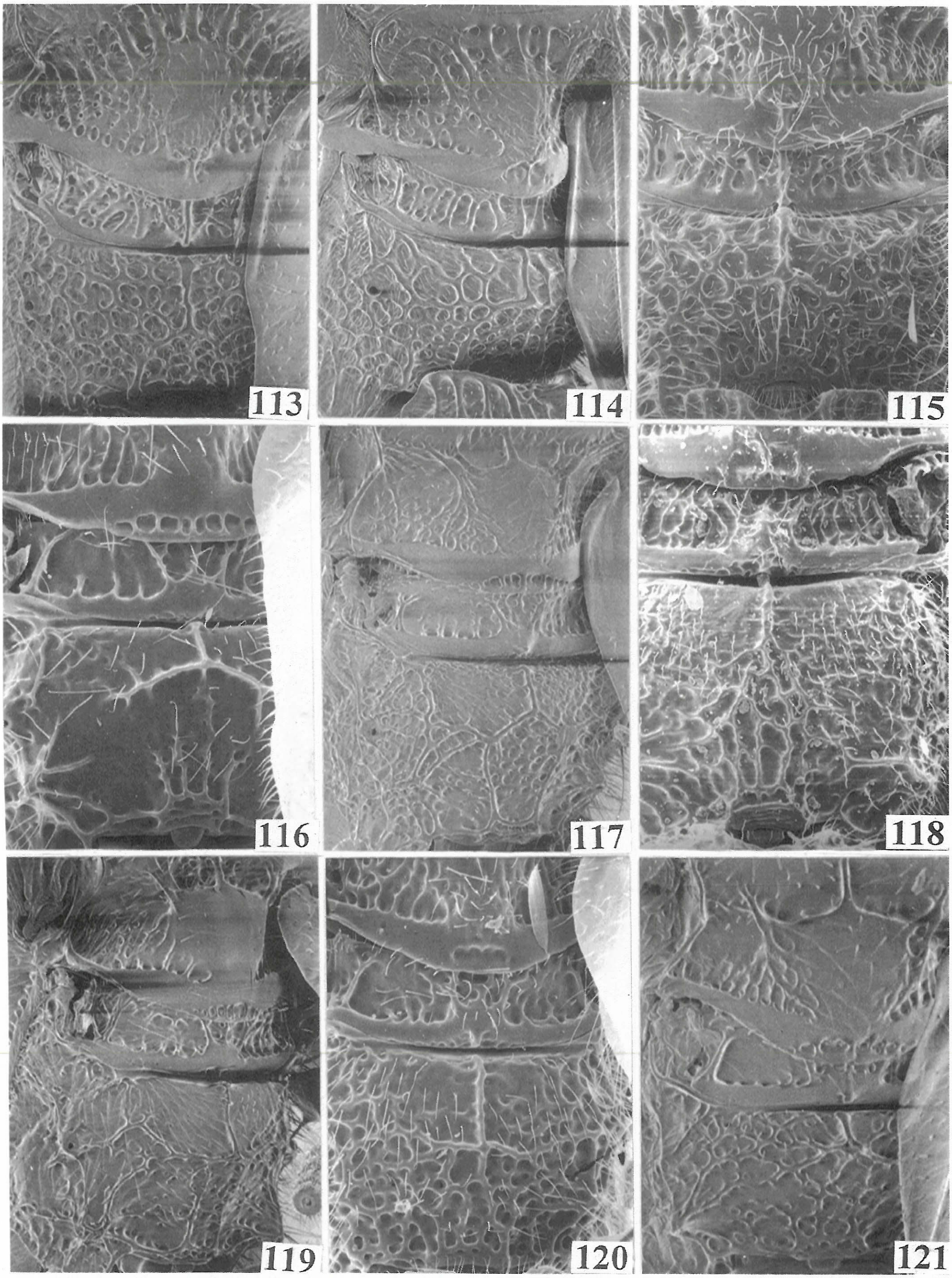


Figs. 95-103. Dorsal view of mesonota of Triaspina ♀: 95, *Triaspis chunji* sp. n.; 96, *T. curvatus* sp. n.; 97, *T. distinctus* sp. n.; 98, *T. fessus* sp. n.; 99, *T. hui* sp. n.; 100, *T. ketiao* sp. n.; 101, *T. kueichia* sp. n.; 102, *T. lienhuachihensis* sp. n.; 103, *T. loi* sp. n.

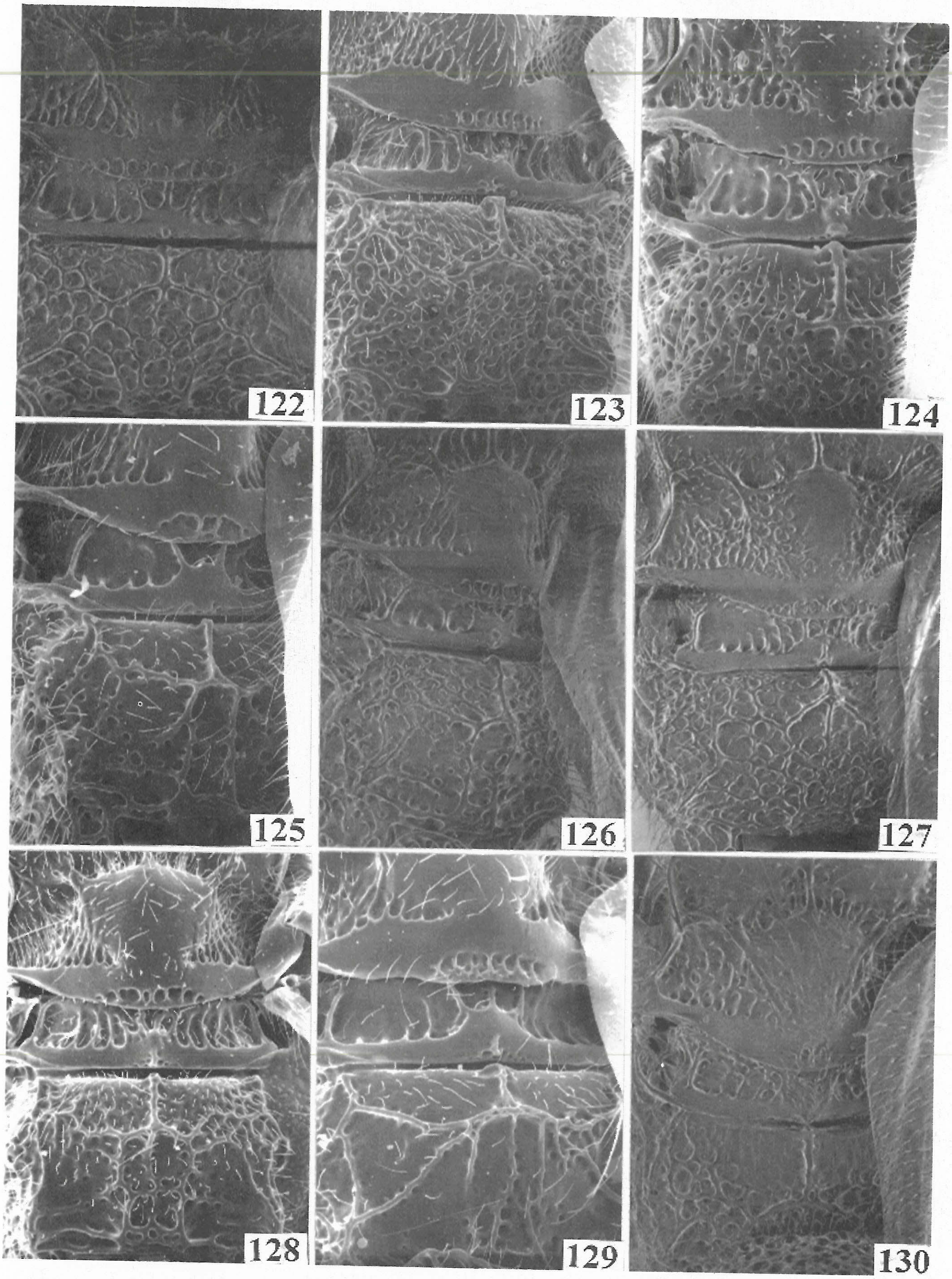


Figs. 104–110. Dorsal view of mesonota of Triaspina ♀: 104, *Triaspis ovatus* sp. n.; 105, *T. plenus* sp. n.; 106, *T. robustus* sp. n.; 107, *T. shan* sp. n.; 108, *T. tungpuensis* sp. n.; 109, *T. concavus* sp. n.; 110, *T. shangchia* sp. n.

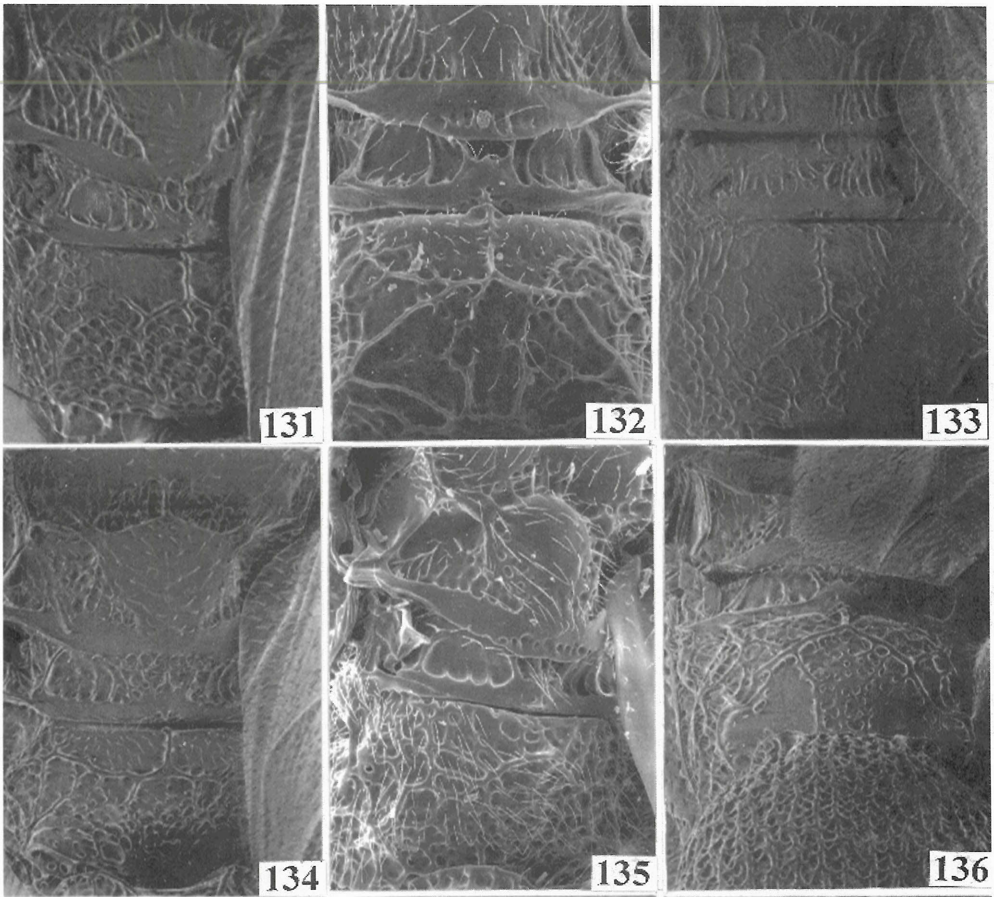
Figs. 111–112. Dorsal view of metanota and propodea of Triaspina ♀: 111, *Triaspis concavus* sp. n.; 112, *T. shangchia* sp. n.

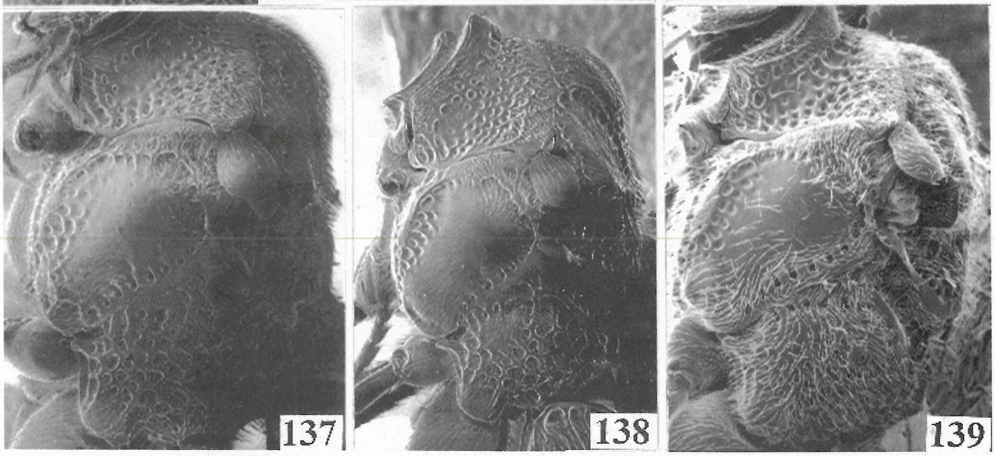


Figs. 113–121. Dorsal view of metanota and propodea of Triaspina ♀: 113, *Canalicephalus fugou* sp. n.; 114, *C. longus* sp. n.; 115, *C. taiwanensis* sp. n.; 116, *T. beitun* sp. n.; 117, *T. bicolor* sp. n.; 118, *T. borpian* sp. n.; 119, *T. calvus* sp. n.; 120, *T. imitatus* Papp; 121, *T. chiu* sp.n.



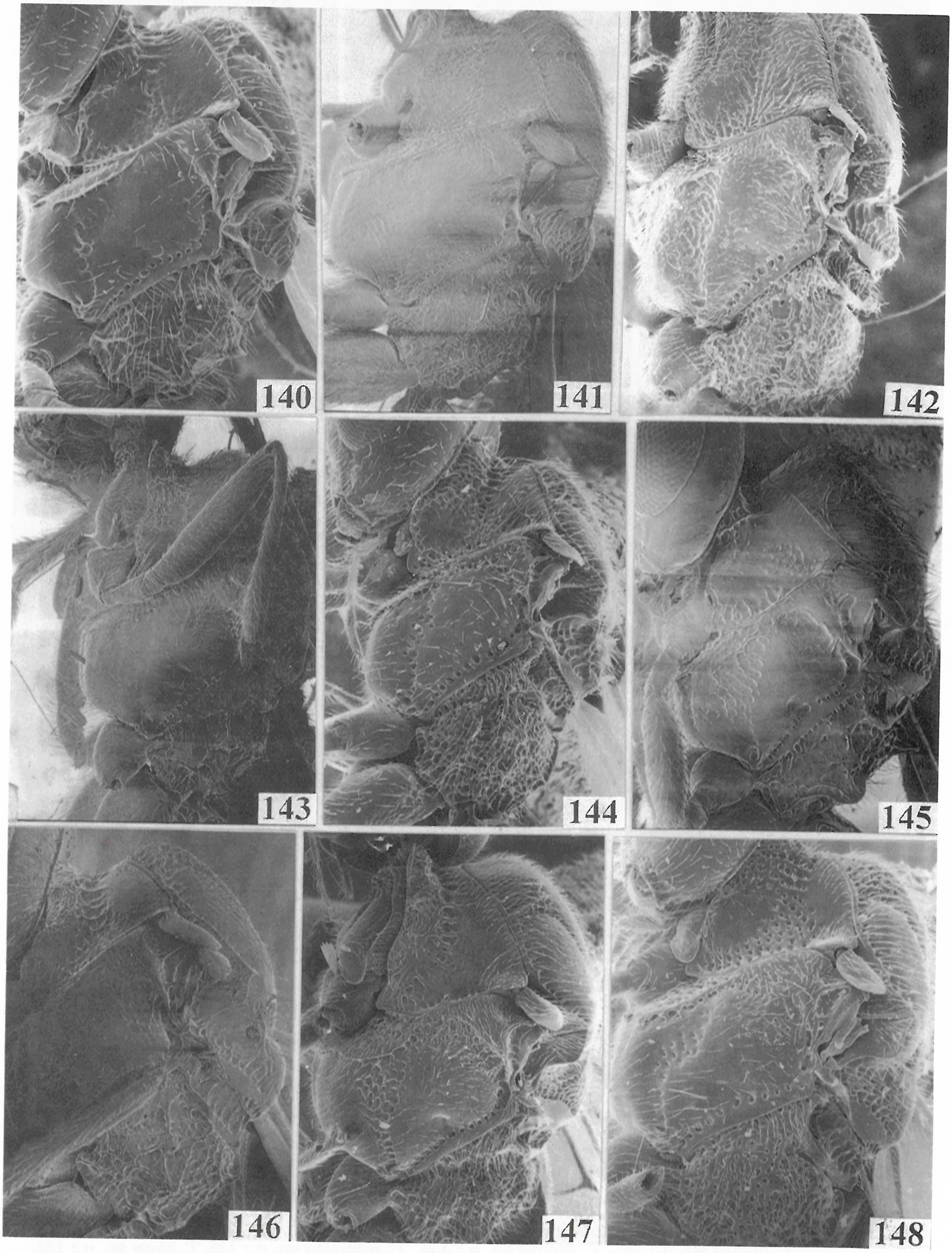
Figs. 122-130. Dorsal view of metanota and propodea of Triaspina ♀: 122, *Triaspis chouwen* sp. n.; 123, *T. chunji* sp. n.; 124, *T. curvatus* sp. n.; 125, *T. distinctus* sp.n.; 126, *T. fessus* sp. n.; 127, *T. hui* sp. n.; 128, *T. ketiao* sp. n.; 129, *T. kueichia* sp. n.; 130, *T. lienhuachihensis* sp.n.



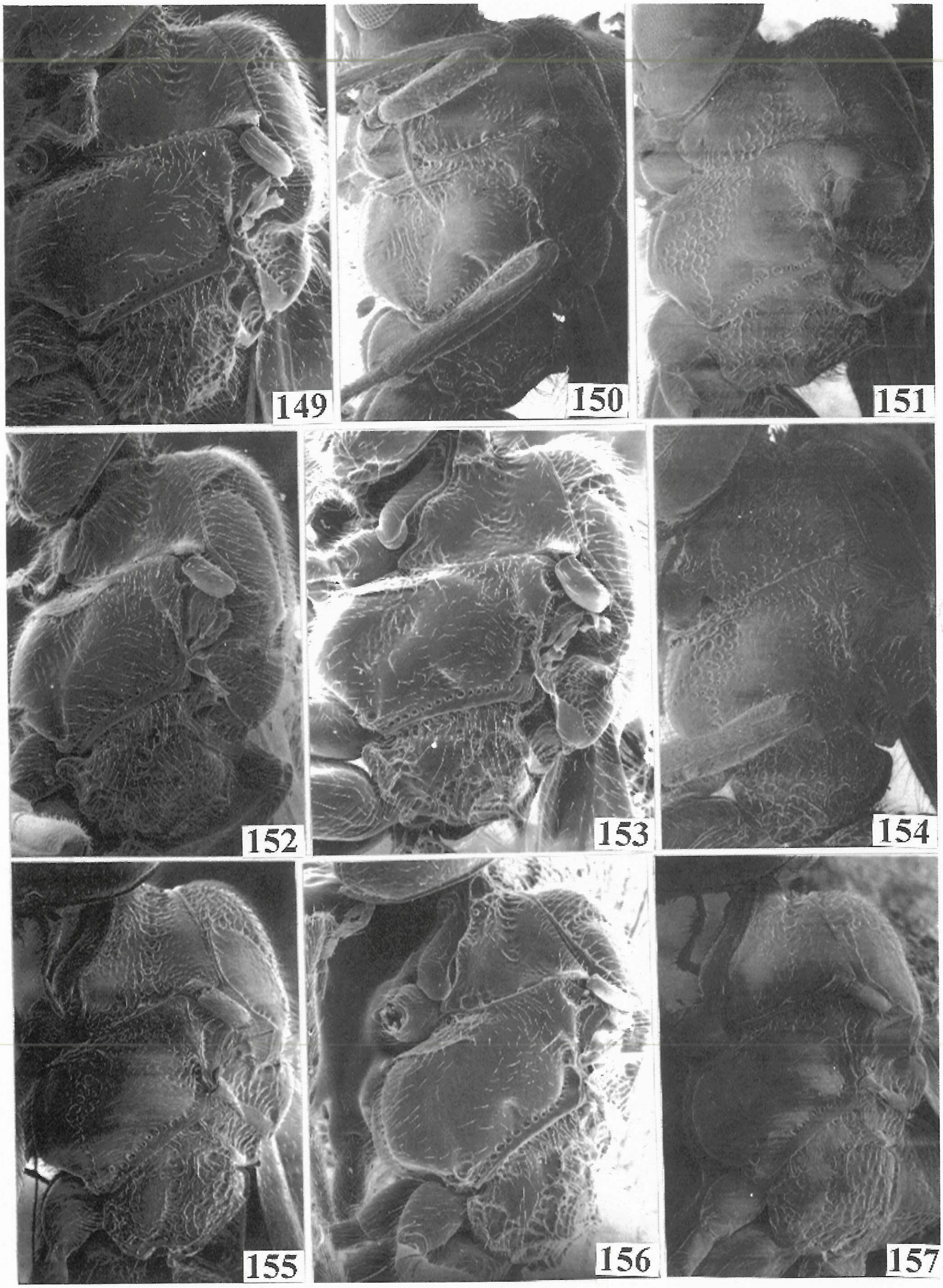


Figs. 131–136. Dorsal view of metanota and propodea of Triaspina ♀: 131, *Triaspis loi* sp. n.; 132, *T. ovatus* sp. n.; 133, *T. plenus* sp. n.; 134, *T. robustus* sp. n.; 135, *T. shan* sp. n.; 136, *T. tungpuensis* sp. n.

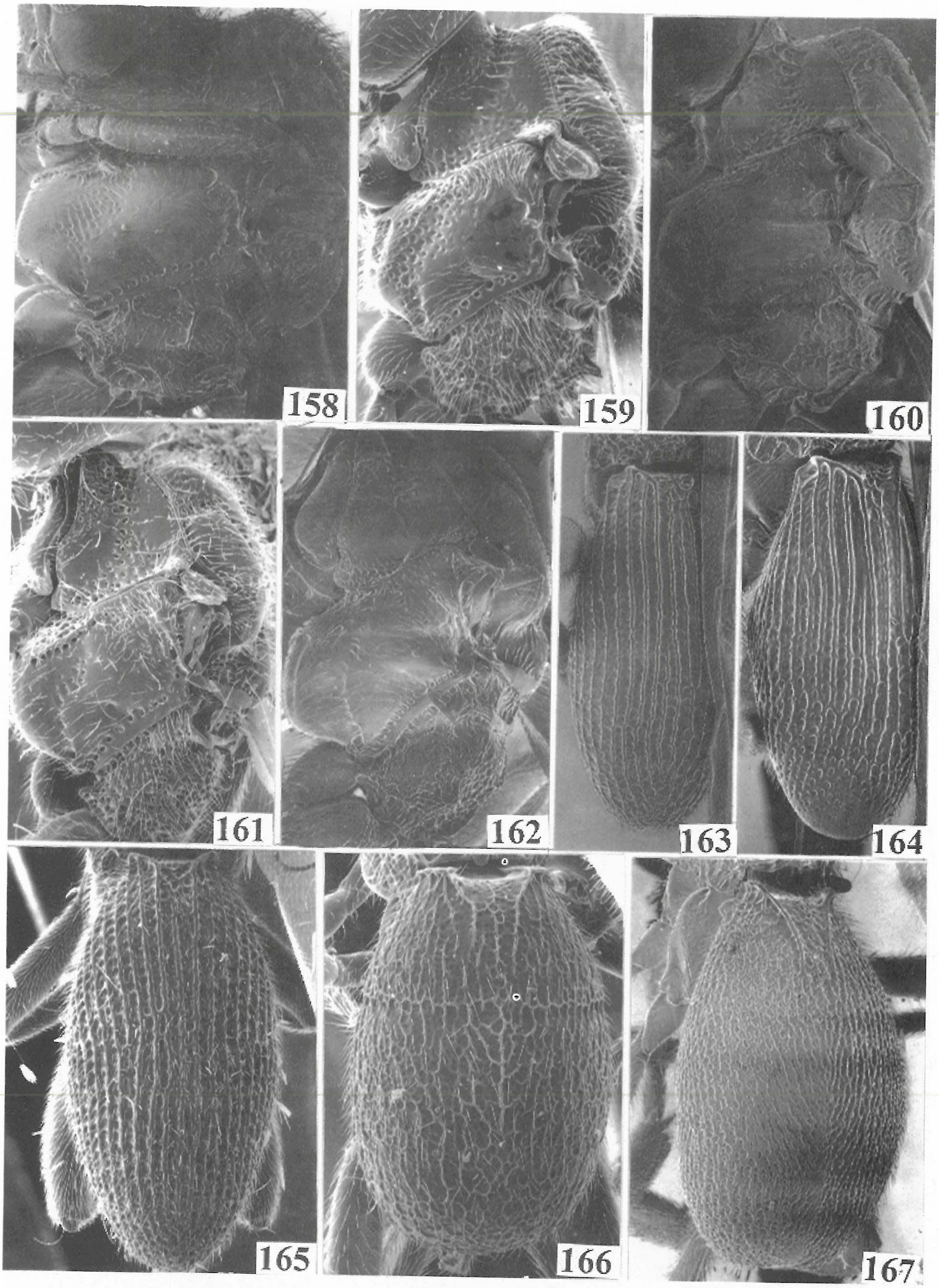
Figs. 137–139. Lateral view of mesosomata of Triaspina ♀: 137, *Canalicephalus fugou* sp. n.; 138, *C. longus* sp. n.; 139, *C. taiwanensis* sp. n.



Figs. 140–148. Lateral view of mesosomata of Triaspina ♀: 140, *Triaspis beitun* sp. n.; 141, *T. bicolor* sp. n.; 142, *T. borpian* sp. n.; 143, *T. calvus* sp. n.; 144, *T. imitatus* Papp; 145, *T. chiu* sp. n.; 146, *T. chouwen* sp. n.; 147, *T. chunji* sp. n.; 148, *T. curvatus* sp. n.

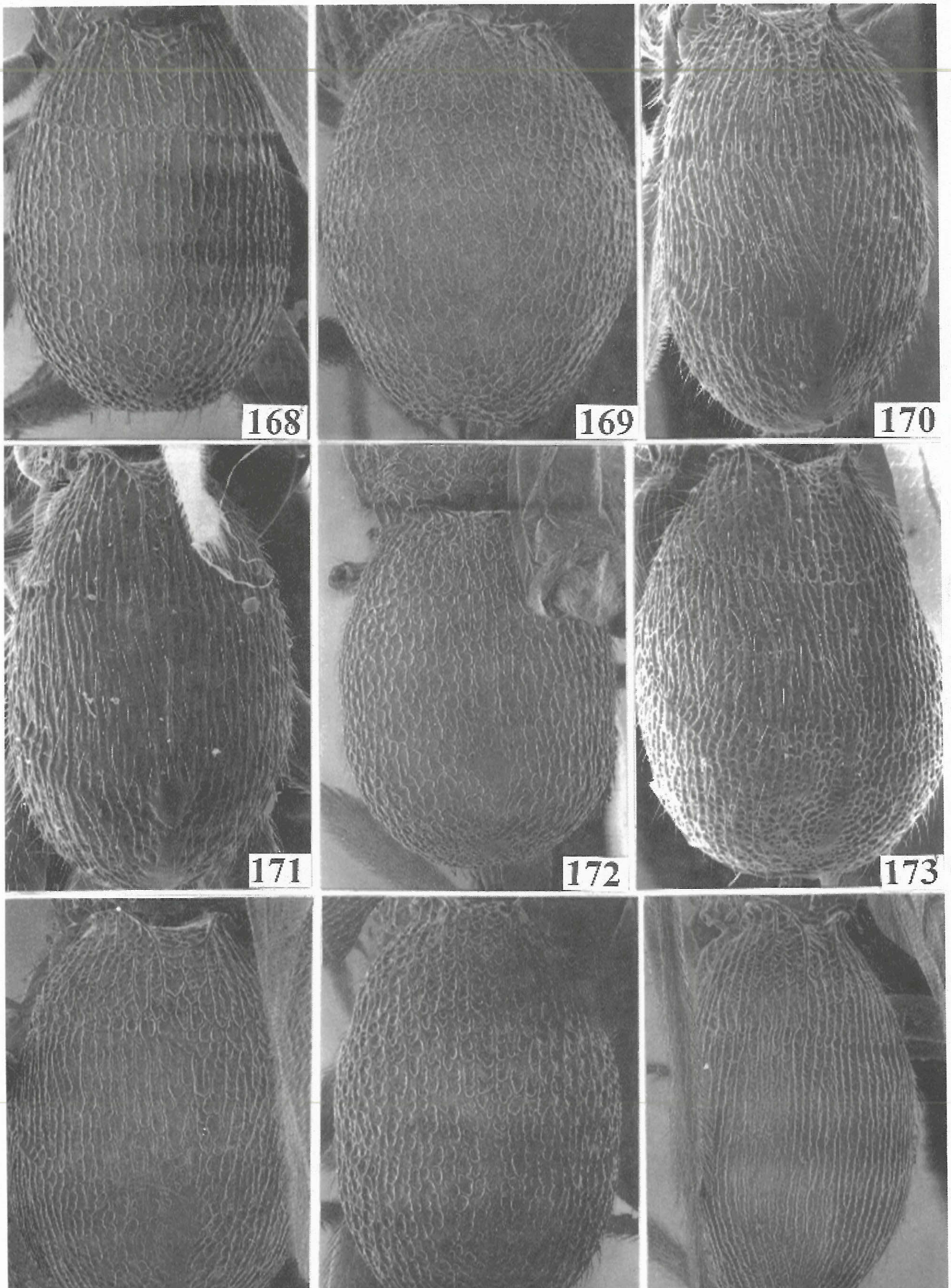


Figs. 149–157. Dorsal view of mesosomata of Triaspina ♀: 149, *Triaspis distinctus* sp. n.; 150, *T. fessus* sp. n.; 151, *T. hui* sp. n.; 152, *T. ketiao* sp. n.; 153, *T. kueichia* sp. n.; 154, *T. lienhuachihensis* sp. n.; 155, *T. loi* sp. n.; 156, *T. ovatus* sp. n.; 157, *T. plenus* sp. n.

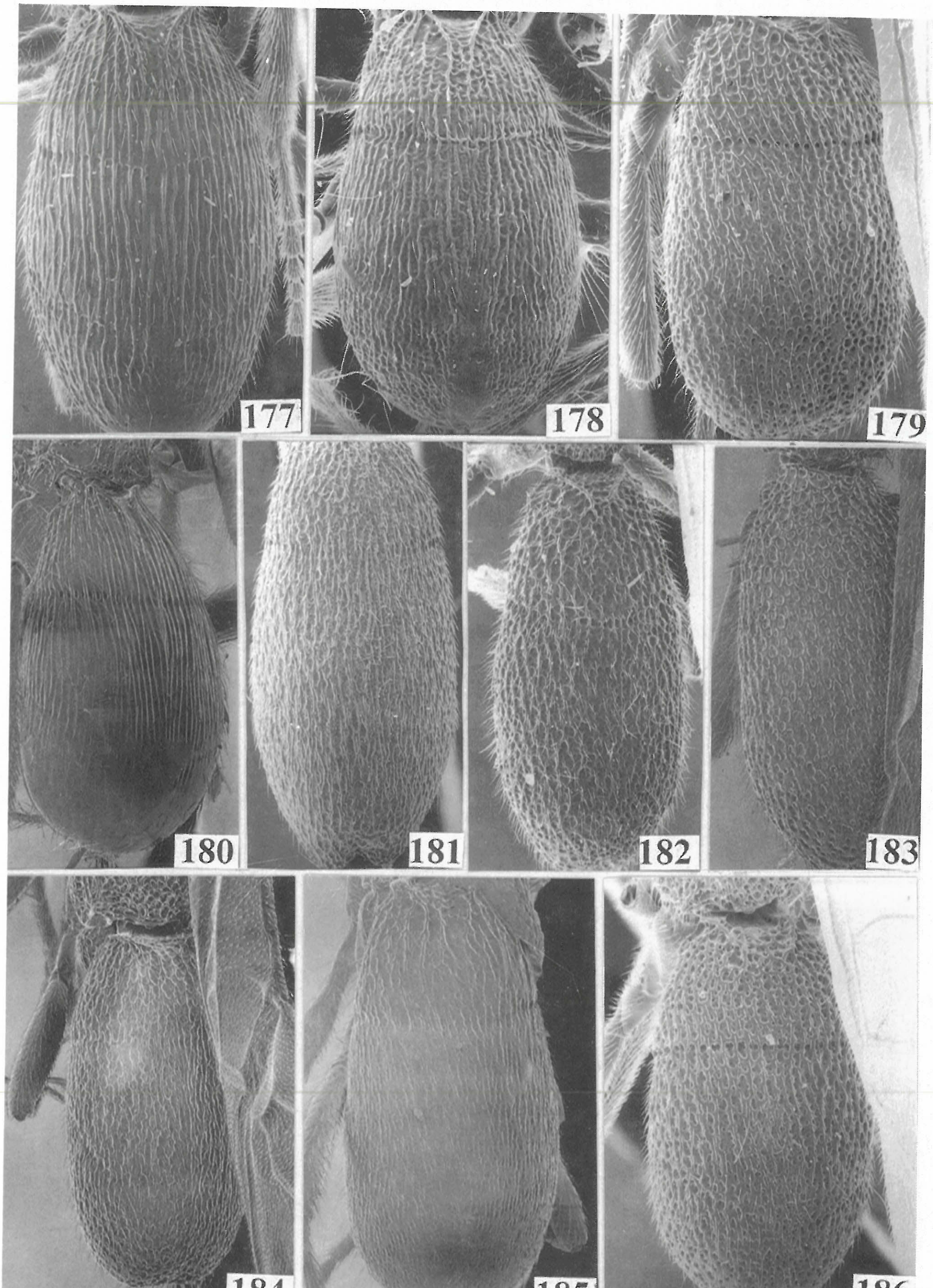


Figs. 158–162. Lateral view of mesosomata of Triaspina ♀: 158, *Triaspis robustus* sp. n.; 159, *T. shan* sp. n.; 160, *T. tungpuensis* sp. n.; 161, *T. concavus* sp. n.; 162, *T. shangchia* sp. n.

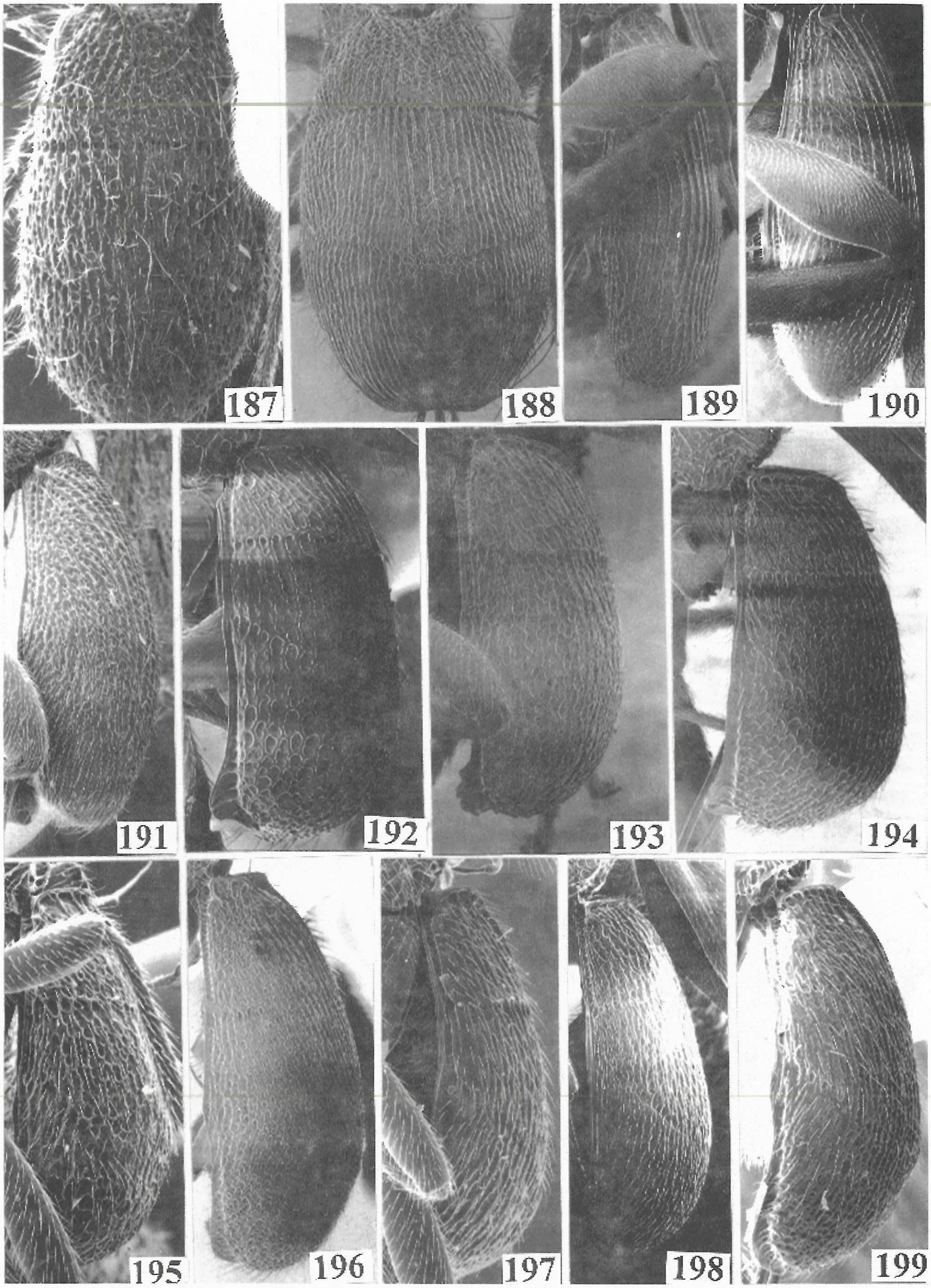
Figs. 163–167. Dorsal view of metasomata of Triaspina ♀: 163, *Canalicephalus fugou* sp. n.; 164, *C. longus* sp. n.; 165, *C. taiwanensis* sp. n.; 166, *T. beitun* sp. n.; 167, *T. bicolor* sp. n.



Figs. 168–176. Dorsal view of metasomata of Triaspina ♀: 168, *Triaspis chiu* sp. n.; 169, *T. chouwen* sp. n.; 170, *T. chunji* sp. n.; 171, *T. distinctus* sp. n.; 172, *T. hui* sp. n.; 173, *T. kueichia* sp. n.; 174, *T. robustus* sp. n.; 175, *T. tungpuensis* sp. n.; 176, *T. fessus* sp. n.

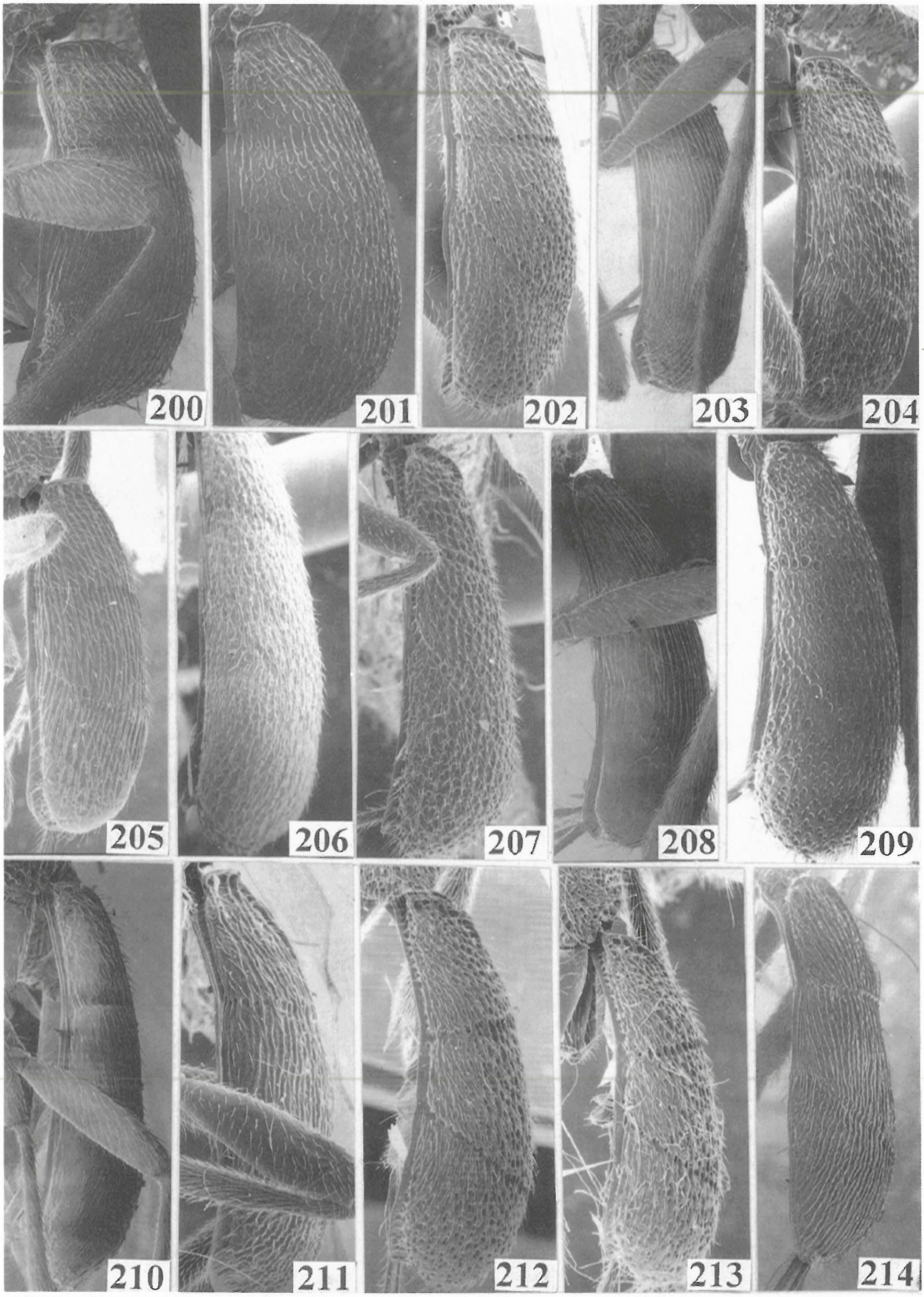


Figs. 177–186. Dorsal view of metasomata of Triaspina ♀: 177, *Triaspis ketiao* sp. n.; 178, *T. ovatus* sp. n.; 179, *T. shan* sp. n.; 180, *T. calvus* sp. n.; 181, *T. borpian* sp. n.; 182, *T. imitatus* Papp; 183, *T. lienhuachihensis* sp. n.; 184, *T. loi* sp. n.; 185, *T. plenus* sp. n.; 186, *T. curvatus* sp. n.

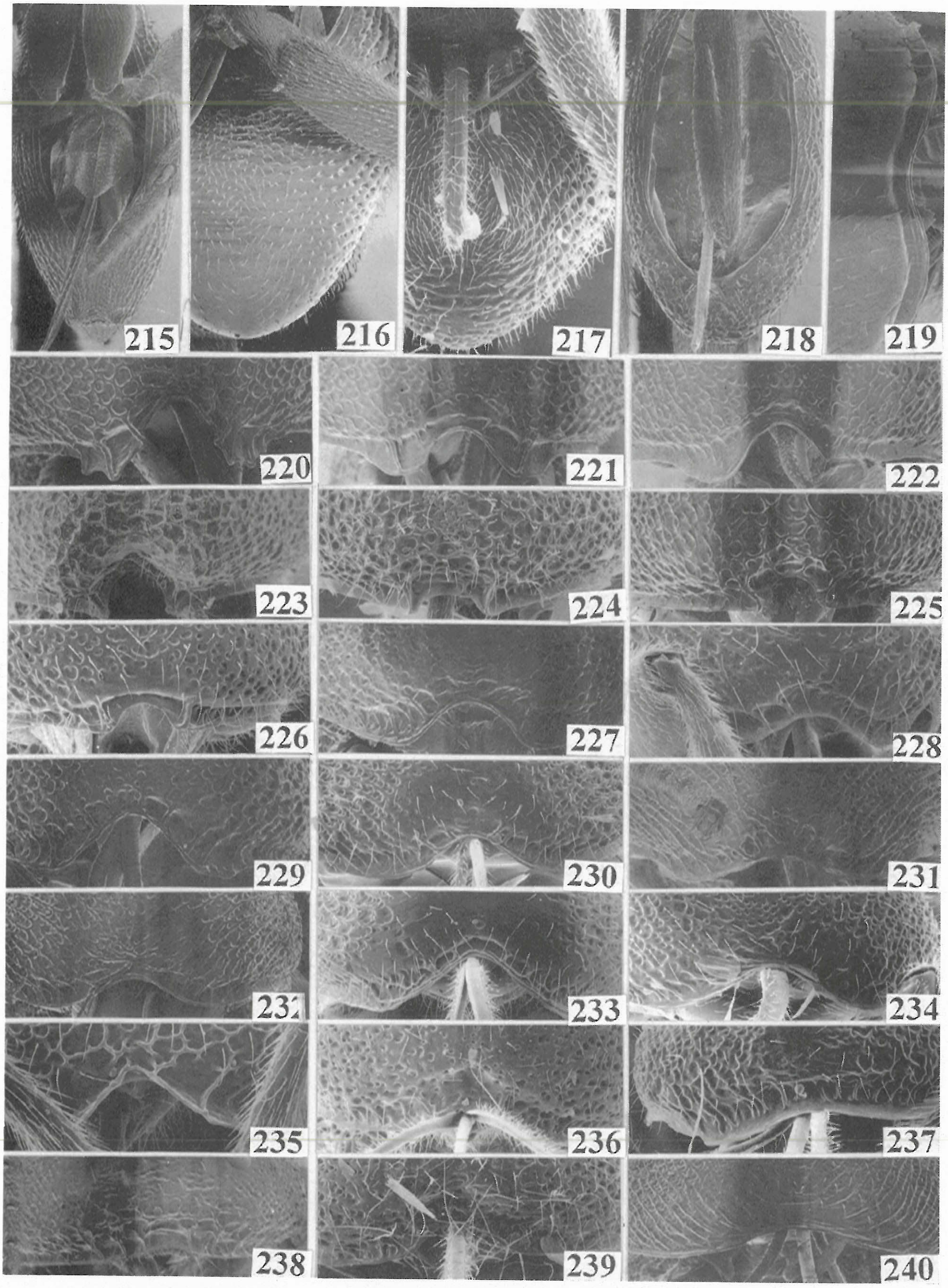


Figs. 187–188. Dorsal view of metasomata of Triaspina ♀: 187, *Triaspis concavus* sp. n.; 188, *T. shangchia* sp. n.

Figs. 189–199. Lateral view of metasomata of Triaspina ♀: 189, *Canalicephalus fugou* sp. n.; 190, *C. longus* sp. n.; 191, *C. taiwanensis* sp. n.; 192, *Triaspis chiu* sp. n.; 193, *T. chouwen* sp. n.; 194, *T. hui* sp. n.; 195, *T. beitun* sp. n.; 196, *T. bicolor* sp. n.; 197, *T. distinctus* sp. n.; 198, *T. loi* sp. n.; 199, *T. kueichia* sp. n.

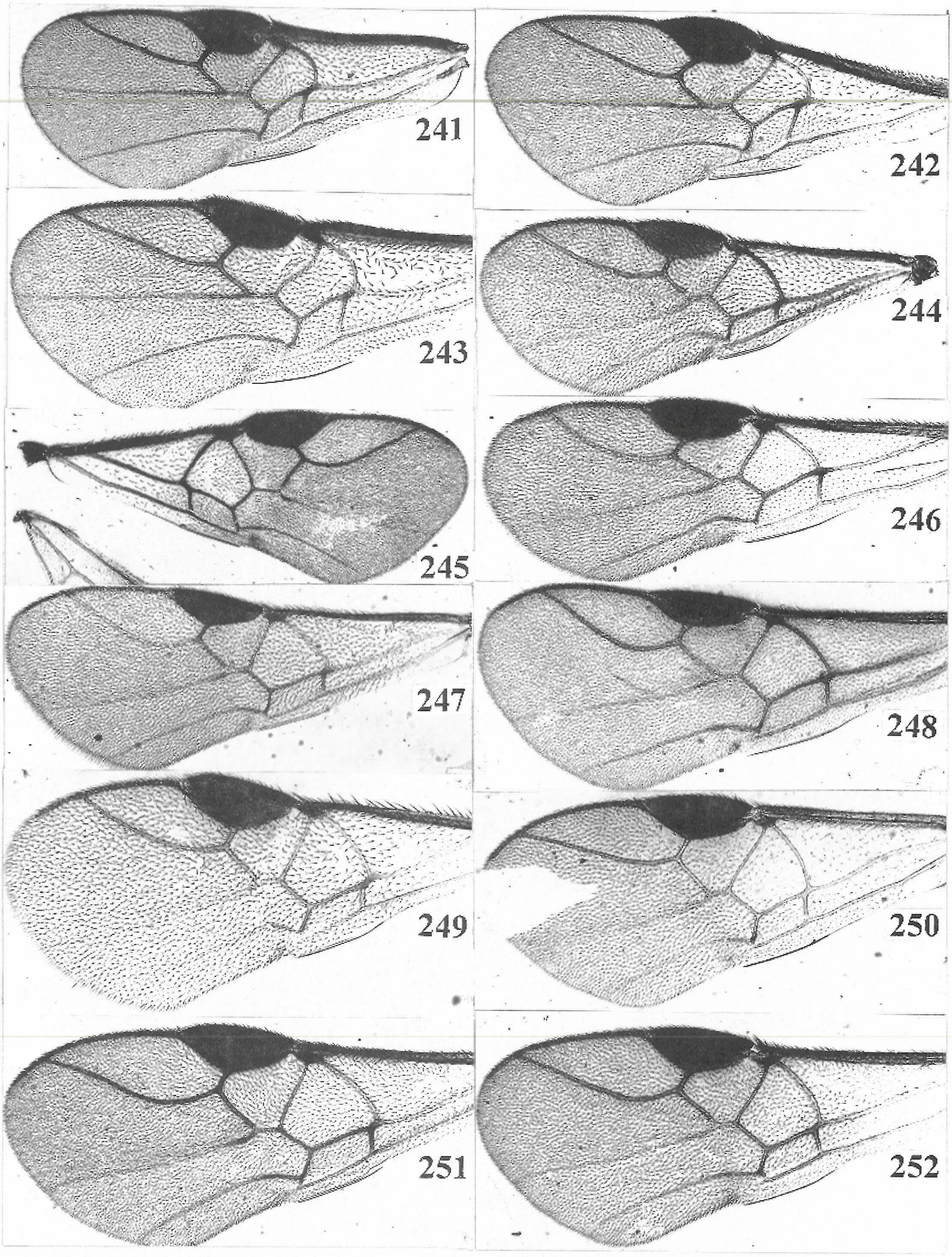


Figs. 200–214. Lateral view of metasomata of Triaspina ♀: 200, *Triaspis robustus* sp. n.; 201, *T. tungpuensis* sp. n.; 202, *T. shan* sp. n.; 203, *T. fessus* sp. n.; 204, *T. chunji* sp. n.; 205, *T. ketiao* sp. n.; 206, *T. borpian* sp. n.; 207, *T. imitatus* Papp; 208, *T. calvus* sp. n.; 209, *T. lienhuachihensis* sp. n.; 210, *T. plenus* sp. n.; 211, *T. ovatus* sp. n.; 212, *T. curvatus* sp. n.; 213, *T. concavus* sp. n.; 214, *T. shangchia* sp. n.

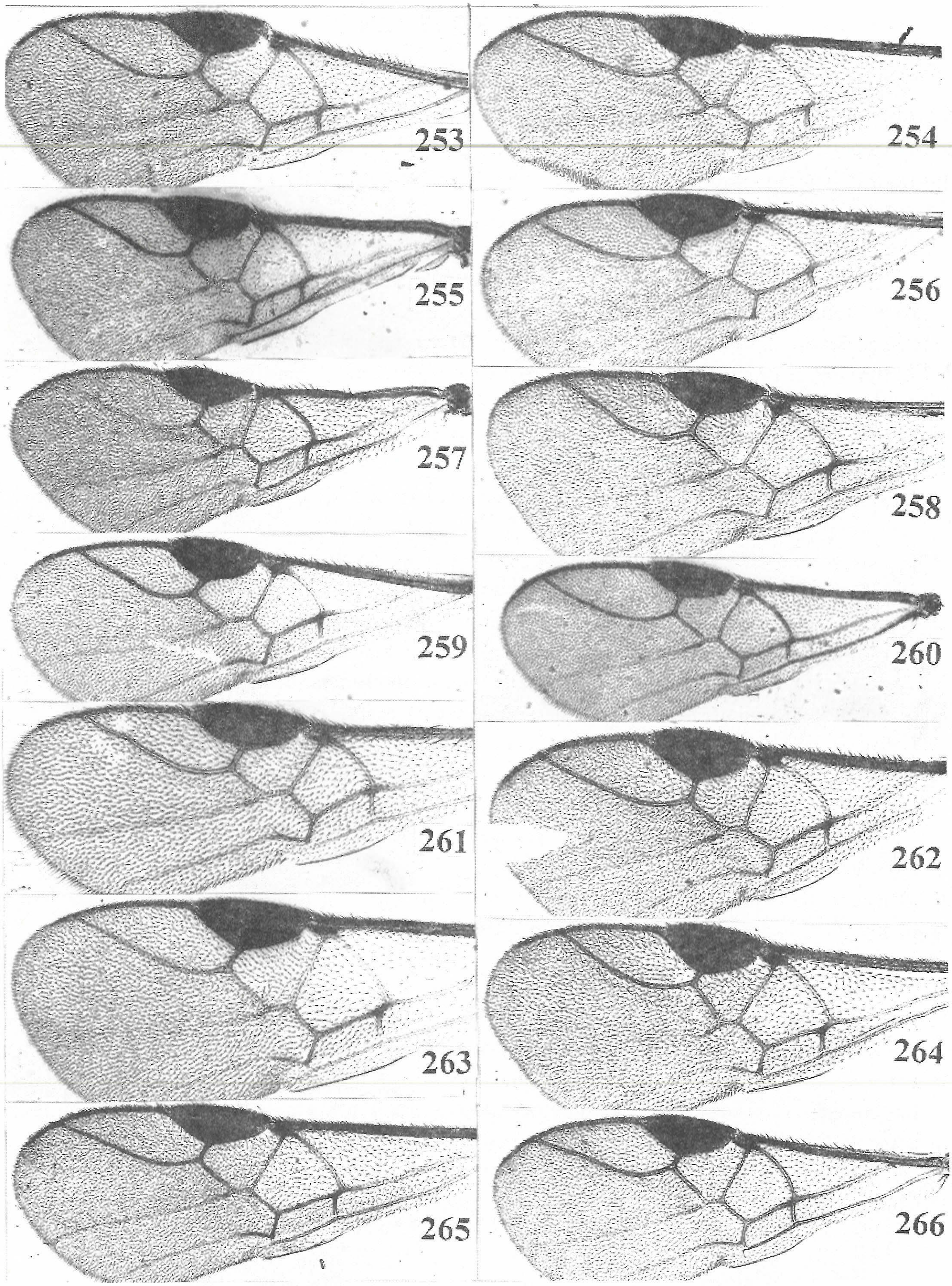


Figs. 215–218. Ventral view of apical metasomata of Triaspina ♀: 215, *Canalicephalus fugou* sp. n.; 216, *C. longus* sp. n.; 217, *C. taiwanensis* sp. n.; 218, *Triaspis lienhuachihensis* sp. n.

Figs. 219–240. Apical end of carapace of Triaspina ♀: 219, *Triaspis calvus* sp. n.; 220, *T. chouwen* sp. n.; 221, *T. chiu* sp. n.; 222, *T. hui* sp. n.; 223, *T. borpian* sp. n.; 224, *T. imitatus* Papp; 225, *T. loi* sp. n.; 226, *T. shan* sp. n.; 227, *T. bicolor* sp. n.; 228, *T. distinctus* sp. n.; 229, *T. tungpuensis* sp. n.; 230, *T. chunji* sp. n.; 231, *T. fessus* sp. n.; 232, *T. robustus* sp. n.; 233, *T. ketiao* sp. n.; 234, *T. kueichia* sp. n.; 235, *T. beitun* sp. n.; 236, *T. curvatus* sp. n.; 237, *T. ovatus* sp. n.; 238, *T. plenus* sp. n.; 239, *T. concavus* sp. n.; 240, *T. shangchia* sp. n.



Figs. 241–252. Forewings of Triaspina ♀: 241, *Canalicephalus fugou* sp. n.; 242, *C. longus* sp. n.; 243, *C. taiwanensis* sp. n.; 244, *Triaspis beitun* sp. n.; 245, *T. bicolor* sp. n.; 246, *T. borpian* sp. n.; 247, *T. calvus* sp. n.; 248, *T. imitatus* Papp; 249, *T. chiu* sp. n.; 250, *T. chouwen* sp. n.; 251, *T. chunji* sp. n.; 252, *T. curvatus* sp. n.



Figs. 253–266. Forewings of Triaspina ♀: 253, *Triaspis distinctus* sp. n.; 254, *T. fessus* sp. n.; 255, *T. hui* sp. n.; 256, *T. ketiao* sp. n.; 257, *T. kueichia* sp. n.; 258, *T. lienhuachihensis* sp. n.; 259, *T. loi* sp. n.; 260, *T. ovatus* sp. n.; 261, *T. plenus* sp. n.; 262, *T. robustus* sp. n.; 263, *T. shan* sp. n.; 264, *T. tungpuensis* sp. n.; 265, *T. shangchia* sp. n.; 266, *T. concavus* sp. n.

ACKNOWLEDGEMENTS

We wish to express our cordial thanks to Dr. Michael J. Sharkey for suggestion about the term "subalar fossa"; to Bishop Museum, Honolulu for the loan of the type specimen of *Schizoprymmus imitatus* Papp; and to American Entomological Institute, Gainesville for the loan of the specimens of *Triaspis*.

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臺灣小繭蜂科（膜翅目）之分類

VII. 三盾繭蜂亞族[1]

周 樑 鎰[2] 許 洞 慶[3]

摘 要

三盾繭蜂亞族（Triaspina）隸膜翅目、小繭蜂科、長繭蜂亞科（Helconinae）、短繭蜂族（Brachistina），全世界已知種類約290種，在臺灣則僅記錄 1 種。本文共描述臺灣產之 3 種凹頂繭蜂（*Canalicephalus*）與22種三盾繭蜂（*Triaspis*）。文中並附分屬與分種檢索表及形質圖。

關鍵詞：三盾繭蜂亞族、長繭蜂亞科、小繭蜂科、分類、臺灣。

1. 臺灣省農業試驗所 研究報告第 1878 號。
2. 本所應用動物系副研究員。臺灣省 臺中縣 霧峰鄉。
3. 國立臺灣大學植物病蟲害學研究所教授。臺北市羅斯福路四段。

中華農業研究稿約

一、本刊爲臺灣省農業試驗所發行之學術性季刊，刊登農業試驗研究相關之研究報告及研究簡報。

二、來稿可用中文或英文撰寫，包括原稿一份及影本二份（內各附照片原圖）。稿件以未在其他刊物發表者爲限。稿紙以 A4紙張（長29.6公分，寬21公分）打字列印，每頁以不超過二十五行爲原則，上下應預留3公分，左右2公分空間，以便審查。

三、來稿經編審委員會審查合格後刊登，由本刊印贈抽印本50本；彩色頁印刷及抽印本加印份數，由投稿人員負擔印製費用。

四、稿件格式請依以下說明繕打：

(一)第一頁爲中文稿之中英文題目、作者之中英文姓名；英文稿之英中文題目、作者之英中文姓名。英文題目除介系詞、連接詞等字外，每字第一字母應大寫；英文姓名：名字在前，姓氏在後，作者二人或二人以上，最後一人前加〝and〞字樣，其表示方法如 Chen-Seng Huang, Chen-Chang Chen and Chyr-Guan Chern。

(二)第二頁爲中（英）文稿之中（英）文摘要與關鍵詞。中、英文摘要均不分段落。中文摘要以不超過五百字，英文摘要（Summary）以不超過三百字爲原則。關鍵詞（Key words）不能超過五個，每個英文關鍵詞第一字母應大寫，其表示方法如 Key words：Heritability, Indirect selection.

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(四)第四頁爲臺灣省農業試驗所研究報告刊登之編號（編號謄空）、作者之註脚，如通信作者、發表場合、服務機關、及其他相關事項等，以小號數字表示順序。

(五)第五頁起爲本文，依序爲前言（INTRODUCTION）、材料與方法（MATERIALS AND METHODS）、結果（RESULTS）、討論（DISCUSSION）、誌謝（ACKNOWLEDGEMENTS，含計畫編號）、引用文獻（REFERENCES）、表、圖之說明（LEGEND）及圖，其中結果及討論兩項可合併爲「結果與討論（RESULTS AND DISCUSSION）」；研究簡報則不分章節，內容簡短，以不超過四印刷頁爲度（約6,000字）。農推、農經研究報告參考本方法書寫。

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2. Hsu, S. H., T. Y. Chung, T. C. Kuo and S. F. Wang. 1992. Studies on the micro-climate of greenhouse. I. Light environment of greenhouse (in Chinese). J. Agric. Assoc. China 157：34-43.
3. Weng, J. H. 1992. CO_2 exchange characteristics of C_3 and C_4 vegetable crops in response to light and nitrogen (in Chinese). J. Agric. Assoc. China 157：21-33.

(2)文獻出自著作性書籍

1. 楊清白。1980。家畜飼料學。74-108頁。藝軒。臺北。
2. Sung, J. M. 1991. Nitrogen Metabolism of Rice. p.100. Chinese Agronomy Press, Taipei.

(3)文獻出自編輯性書籍

1. Lo, W. S. 1991.The effect of calcium on nitrogen metabolism pp. 100—110. in: Biology of Rice. (Sung, J. M. and D. J. Liu, eds.) Chinese Agronomy Press, Taipei.

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